



SEQUENCE LISTING

<110> COLE, STEWART
BROSCH, ROLAND
GORDON, STEPHEN
EIGLMEIER, KARIN
GARNIER, THIERRY

<120> DELETED SEQUENCE IN M. TUBERCULOSIS, METHOD FOR DETECTING
MYCOBACTERIA USING THESE SEQUENCES AND VACCINES

<130> 05394.0020

<140> 10/505,405

<141> 2006-01-13

<150> PCT/IB03/00986

<151> 2003-02-25

<150> EP 02290458.5

<151> 2002-02-25

<160> 117

<170> PatentIn version 3.5

<210> 1

<211> 3953

<212> DNA

<213> Mycobacterium tuberculosis

<220>

<221> CDS

<222> (735)..(3638)

<400> 1

tccagcgcgg ccatcagcga tgaactctgg gacctgctac ccggctacct catcttccgg	60
tccatcatcc ccaaccggcc gccacccag gacacgggtgc aagccctcgt cgacgacgtg	120
atactcccca gcctcaccgg atccaccggt tgagtcagcg gtgcgaatgg ctggggaccg	180
ttgtggtgtc cgggtcccgt cgtactgtt gaatccgcgg atccccgcct gaggtacggg	240
gcgtggtcgc gccccgggca atagcgtcgc cggttatcga aaggctaacg ggtgcagggg	300
atttcagtga ctggcctggt caaacgcggc tggatggtgc tggttgccgt ggcggtggtg	360
gcggtcgcgg gattcagcgt ctatcggttg cacggcatct tcggctcgca cgacaccacc	420
tcgaccgccg gtggtgtcgc gaacgacatc aagccgttca accccaaaca ggtaaccctc	480
gaggtctttg gcgctcccgg aaccgtggca acgatcaatt atctggacgt ggatgccaca	540
cctcggcaag tcctggacac gaccctgccg tggtcataca cgatcacgac gaccctgccc	600
gcggtcttcg ccaatgttgt cgcgcaaggc gacagcaatt ccatcggctg ccgcatcacc	660

gtcaacgggtg tagtcaagga cgaaaggatc gtcaacgaag tgcgcgccta taccttctgc	720
ctcgacaagt cctc atg agc aac cac cac cgc ccg cgg cct tgg ttg ccg Met Ser Asn His His Arg Pro Arg Pro Trp Leu Pro 1 5 10	770
cac acc atc cga cgg ctt tcg ttg ccg atc ttg ctg ttt tgg gtg ggt His Thr Ile Arg Arg Leu Ser Leu Pro Ile Leu Leu Phe Trp Val Gly 15 20 25	818
gtg gcc gcc ata acc aat gcc gcc gtg ccg caa ttg gag gtg gtc ggg Val Ala Ala Ile Thr Asn Ala Ala Val Pro Gln Leu Glu Val Val Gly 30 35 40	866
gag gcg cat aac gtc gca cag agc tcc ccg gat gac ccg tcg ctg cag Glu Ala His Asn Val Ala Gln Ser Ser Pro Asp Asp Pro Ser Leu Gln 45 50 55 60	914
gcg atg aaa cgc atc ggc aag gtg ttc cac gag ttc gat tcc gac agt Ala Met Lys Arg Ile Gly Lys Val Phe His Glu Phe Asp Ser Asp Ser 65 70 75	962
gcg gcc atg atc gtc ttg gaa ggc gat aag ccg ctc ggc aac gac gcc Ala Ala Met Ile Val Leu Glu Gly Asp Lys Pro Leu Gly Asn Asp Ala 80 85 90	1010
cac ccg ttc tac gac acc ctg ctc cgc aac ctt tca aac gac acc aaa His Arg Phe Tyr Asp Thr Leu Arg Asn Leu Ser Asn Asp Thr Lys 95 100 105	1058
cac gtc gag cac gtt cag gac ttc tgg ggc gat ccg ctg acc gcg gcc His Val Glu His Val Gln Asp Phe Trp Gly Asp Pro Leu Thr Ala Ala 110 115 120	1106
ggc tcg caa agc acc gac ggc aaa gcc gcc tac gtt cag gtc tat ctc Gly Ser Gln Ser Thr Asp Gly Lys Ala Ala Tyr Val Gln Val Tyr Leu 125 130 135 140	1154
gcc ggc aac caa ggc gag gcg ttg tca atc gag tcc gtc gac gcg gtg Ala Gly Asn Gln Gly Glu Ala Leu Ser Ile Glu Ser Val Asp Ala Val 145 150 155	1202
cgc gac atc gtc gcc cat acg cca cca ccg gcc ggg gtc aag gcc tac Arg Asp Ile Val Ala His Thr Pro Pro Pro Ala Gly Val Lys Ala Tyr 160 165 170	1250
gtc acc ggc gcg gcc ccg ctc atg gcc gat cag ttt cag gtg ggc agc Val Thr Gly Ala Ala Pro Leu Met Ala Asp Gln Phe Gln Val Gly Ser 175 180 185	1298
aaa gga acc gcg aaa gtt acc ggg ata act ctg gtt gtg atc gcg gtg Lys Gly Thr Ala Lys Val Thr Gly Ile Thr Leu Val Val Ile Ala Val 190 195 200	1346
atg ttg ctc ttc gta tac cgt tcc gtc gtc acc atg gtc ctg gtg ctt Met Leu Leu Phe Val Tyr Arg Ser Val Val Thr Met Val Leu Val Leu 205 210 215 220	1394

atc acg gtt ctt att gag ttg gcc gcg gcc cgc ggg atc gtc gct ttt Ile Thr Val Leu Ile Glu Leu Ala Ala Ala Arg Gly Ile Val Ala Phe 225 230 235	1442
ctc gga aac gcc ggg gta atc ggg ctg tcg aca tac tcg acg aat ctg Leu Gly Asn Ala Gly Val Ile Gly Leu Ser Thr Tyr Ser Thr Asn Leu 240 245 250	1490
ctc aca cta ttg gta atc gcg gcg ggc aca gac tac gcg att ttt gtc Leu Thr Leu Leu Val Ile Ala Ala Gly Thr Asp Tyr Ala Ile Phe Val 255 260 265	1538
ctc ggc cgc tat cac gag gcg cgc tac gcc gca cag gat cgg gaa acg Leu Gly Arg Tyr His Glu Ala Arg Tyr Ala Ala Gln Asp Arg Glu Thr 270 275 280	1586
gcc ttc tac acg atg tat cgc ggg acc gcc cac gtc gtc ttg ggc tcg Ala Phe Tyr Thr Met Tyr Arg Gly Thr Ala His Val Val Leu Gly Ser 285 290 295 300	1634
ggt ctg acc gtt gcc ggc gcg gtg tat tgc ctg agc ttt acc cgg cta Gly Leu Thr Val Ala Gly Ala Val Tyr Cys Leu Ser Phe Thr Arg Leu 305 310 315	1682
ccc tat ttt caa agc ctg ggt att ccc gcc tcg ata ggg gtg atg att Pro Tyr Phe Gln Ser Leu Gly Ile Pro Ala Ser Ile Gly Val Met Ile 320 325 330	1730
gcg ttg gca gcc gcg ctc agc ctg gcc cca tcc gtg ctc atc ttg ggc Ala Leu Ala Ala Ala Leu Ser Leu Ala Pro Ser Val Leu Ile Leu Gly 335 340 345	1778
agt cgt ttc ggt tgt ttc gaa ccc aag cgc agg atg agg acc agg gga Ser Arg Phe Gly Cys Phe Glu Pro Lys Arg Arg Met Arg Thr Arg Gly 350 355 360	1826
tgg cgg cgc atc ggc acg gcc atc gtg cgt tgg ccg gga ccc atc ctg Trp Arg Arg Ile Gly Thr Ala Ile Val Arg Trp Pro Gly Pro Ile Leu 365 370 375 380	1874
gca gtg gcg tgc gca att gcg gtg gtg ggt ctg ctc gcg ctg ccg gga Ala Val Ala Cys Ala Ile Ala Val Val Gly Leu Leu Ala Leu Pro Gly 385 390 395	1922
tac aaa acg agc tac gac gct cgc tat tac atg ccc gcc acc gcc ccg Tyr Lys Thr Ser Tyr Asp Ala Arg Tyr Tyr Met Pro Ala Thr Ala Pro 400 405 410	1970
gcc aat att ggc tac atg gcc gcg gag cga cat ttt ccc caa gcg cgg Ala Asn Ile Gly Tyr Met Ala Ala Glu Arg His Phe Pro Gln Ala Arg 415 420 425	2018
ctg aat ccc gaa cta ctg atg atc gag acg gat cac gat atg cgc aat Leu Asn Pro Glu Leu Leu Met Ile Glu Thr Asp His Asp Met Arg Asn 430 435 440	2066

ccg gcc gac atg ctc atc ttg gat agg atc gcc aag gct gtc ttc cat	2114
Pro Ala Asp Met Leu Ile Leu Asp Arg Ile Ala Lys Ala Val Phe His	
445 450 455 460	
ctg ccc ggc ata ggg ctg gtg cag gcc atg acc cgg ccg cta gga acc	2162
Leu Pro Gly Ile Gly Leu Val Gln Ala Met Thr Arg Pro Leu Gly Thr	
465 470 475	
ccg att gac cac agc tcg ata ccg ttt cag atc agc atg caa agc gtc	2210
Pro Ile Asp His Ser Ser Ile Pro Phe Gln Ile Ser Met Gln Ser Val	
480 485 490	
ggc cag att cag aat ctc aag tat cag agg gac cga gca gcc gac ttg	2258
Gly Gln Ile Gln Asn Leu Lys Tyr Gln Arg Asp Arg Ala Ala Asp Leu	
495 500 505	
ctg aag cag gcc gaa gag ctg ggg aag acg atc gaa atc ttg cag cgc	2306
Leu Lys Gln Ala Glu Glu Leu Gly Lys Thr Ile Glu Ile Leu Gln Arg	
510 515 520	
caa tat gcc cta cag cag gaa ctc gcg gcc gct act cac gag caa gcc	2354
Gln Tyr Ala Leu Gln Gln Glu Leu Ala Ala Ala Thr His Glu Gln Ala	
525 530 535 540	
gaa agc ttt cac caa acg atc gcc acg gta aac gaa ctg cga gat agg	2402
Glu Ser Phe His Gln Thr Ile Ala Thr Val Asn Glu Leu Arg Asp Arg	
545 550 555	
atc gcc aat ttc gac gat ttc ttc agg ccg att cgt agt tac ttt tac	2450
Ile Ala Asn Phe Asp Asp Phe Phe Arg Pro Ile Arg Ser Tyr Phe Tyr	
560 565 570	
tgg gaa aag cac tgc tac gat atc ccg agc tgc tgg gcg ctg aga tcc	2498
Trp Glu Lys His Cys Tyr Asp Ile Pro Ser Cys Trp Ala Leu Arg Ser	
575 580 585	
gtc ttt gac acg atc gac ggt atc gac caa ctc ggc gag cag ctg gcc	2546
Val Phe Asp Thr Ile Asp Gly Ile Asp Gln Leu Gly Glu Gln Leu Ala	
590 595 600	
agc gtg acc gta acc ttg gac aag ttg gct gcg atc cag cct caa ttg	2594
Ser Val Thr Val Thr Leu Asp Lys Leu Ala Ala Ile Gln Pro Gln Leu	
605 610 615 620	
gtg gcg ctg cta cca gac gag atc gcc agc cag cag atc aat cgg gaa	2642
Val Ala Leu Leu Pro Asp Glu Ile Ala Ser Gln Gln Ile Asn Arg Glu	
625 630 635	
ctg gcg ctg gct aac tac gcc acc atg tcc ggg atc tat gcc cag acg	2690
Leu Ala Leu Ala Asn Tyr Ala Thr Met Ser Gly Ile Tyr Ala Gln Thr	
640 645 650	
gcg gcc ttg atc gaa aac gct gcc gcc atg gga caa gcc ttt gac gcc	2738
Ala Ala Leu Ile Glu Asn Ala Ala Ala Met Gly Gln Ala Phe Asp Ala	
655 660 665	

gcc aag aac gac gac tcc ttc tat ctg ccg ccg gag gct ttt gac aac Ala Lys Asn Asp Asp Ser Phe Tyr Leu Pro Pro Glu Ala Phe Asp Asn 670 675 680	2786
cca gat ttc cag cgc ggc ctg aaa ttg ttc ctg tcg gca gac ggt aag Pro Asp Phe Gln Arg Gly Leu Lys Leu Phe Leu Ser Ala Asp Gly Lys 685 690 695 700	2834
gcg gct cgg atg atc atc tcc cat gaa ggc gat ccc gcc acc ccc gaa Ala Ala Arg Met Ile Ile Ser His Glu Gly Asp Pro Ala Thr Pro Glu 705 710 715	2882
ggc att tcg cat atc gac gcg atc aag cag gcg gcc cac gag gcc gtg Gly Ile Ser His Ile Asp Ala Ile Lys Gln Ala Ala His Glu Ala Val 720 725 730	2930
aag ggc act ccc atg gcg ggt gct ggg atc tat ctg gcc ggc acg gcc Lys Gly Thr Pro Met Ala Gly Ala Gly Ile Tyr Leu Ala Gly Thr Ala 735 740 745	2978
gcc acc ttc aag gac att caa gac ggc gcc acc tac gac ctc ctg atc Ala Thr Phe Lys Asp Ile Gln Asp Gly Ala Thr Tyr Asp Leu Leu Ile 750 755 760	3026
gcc gga ata gcc gcg ctg agc ttg att ttg ctc atc atg atg atc att Ala Gly Ile Ala Ala Leu Ser Leu Ile Leu Leu Ile Met Met Ile Ile 765 770 775 780	3074
acc cga agc ctg gtt gcg gcg ctg gtg atc gtg ggc acg gtg gcg ctg Thr Arg Ser Leu Val Ala Ala Leu Val Ile Val Gly Thr Val Ala Leu 785 790 795	3122
tcg ttg ggc gct tct ttt ggc ctg tcc gtg ctg gtg tgg cag cat ctt Ser Leu Gly Ala Ser Phe Gly Leu Ser Val Leu Val Trp Gln His Leu 800 805 810	3170
ctc ggt atc cag ttg tac tgg atc gtg ctc gcg ctg gcc gtc atc ctg Leu Gly Ile Gln Leu Tyr Trp Ile Val Leu Ala Leu Ala Val Ile Leu 815 820 825	3218
ctc ctg gcc gtg gga tcg gac tat aac ttg ctg ctg att tcc cga ttc Leu Leu Ala Val Gly Ser Asp Tyr Asn Leu Leu Leu Ile Ser Arg Phe 830 835 840	3266
aag gag gag atc ggt gca ggt ttg aac acc ggc atc atc cgt gcg atg Lys Glu Glu Ile Gly Ala Gly Leu Asn Thr Gly Ile Ile Arg Ala Met 845 850 855 860	3314
gcc ggc acc ggc ggg gtg gtg acc gct gcc ggc ctg gtg ttc gcc gcc Ala Gly Thr Gly Gly Val Val Thr Ala Ala Gly Leu Val Phe Ala Ala 865 870 875	3362
act atg tct tcg ttc gtg ttc agt gat ttg cgg gtc ctc ggt cag atc Thr Met Ser Ser Phe Val Phe Ser Asp Leu Arg Val Leu Gly Gln Ile 880 885 890	3410

ggg acc acc att ggt ctt ggg ctg ctg ttc gac acg ctg gtg gtg cgc 3458
Gly Thr Thr Ile Gly Leu Gly Leu Leu Phe Asp Thr Leu Val Val Arg
895 900 905

gcg ttc atg acc ccg tcc atc gcg gtg ctg ctc ggg cgc tgg ttc tgg 3506
Ala Phe Met Thr Pro Ser Ile Ala Val Leu Leu Gly Arg Trp Phe Trp
910 915 920

tgg ccg caa cga gtg cgc ccg cgc cct gcc agc agg atg ctt cgg ccg 3554
 Trp Pro Gln Arg Val Arg Pro Arg Pro Ala Ser Arg Met Leu Arg Pro
 925 930 935 940

tac	ggc	ccg	cgg	ccc	gtg	gtt	cgt	gaa	ttg	ctg	ctg	cgc	gag	ggc	aac	3602
Tyr	Gly	Pro	Arg	Pro	Val	Val	Arg	Glu	Leu	Leu	Leu	Arg	Glu	Gly	Asn	
				945					950					955		

gat gac ccg aga act cag gtg gct acc cac cgt taa ggtgggtggga 3648
Asp Asp Pro Arg Thr Gln Val Ala Thr His Arg
960 965

tgccgctttc aggggaatat gcgccgagcc cgctcgactg gtcgcgcgag caagccgaca 3708

cgtatatgaa gtccggcgga accgagggca cacagctgca gggaaagccg gtcattctgc 3768

tcaccaccgt cggggcgaaq accggcaaac tccgtaagac cccgctgatg cgcgtcgagc 3828

acgacggcca gtacgcgata gtcgcctcgc tgggtggggc gccgaaaaat ccggtctggt 3888

accacaacgt cgtgaagaac ccacgggtcg agctgcagga cggcaccgga ccggcgacta 3948

cgacg 3953

```
<210> 2
<211> 967
<212> PRT
<213> Mycobacterium tuberculosis
```

<400> 2
Met Ser Asn His His Arg Pro Arg Pro Trp Leu Pro His Thr Ile Arg
1 5 10 15

Arg Leu Ser Leu Pro Ile Leu Leu Phe Trp Val Gly Val Ala Ala Ile
20 25 30

Thr Asn Ala Ala Val Pro Gln Leu Glu Val Val Gly Glu Ala His Asn
35 40 45

Val Ala Gln Ser Ser Pro Asp Asp Pro Ser Leu Gln Ala Met Lys Arg
50 55 60

Ile Gly Lys Val Phe His Glu Phe Asp Ser Asp Ser Ala Ala Met Ile
65 70 75 80

Val Leu Glu Gly Asp Lys Pro Leu Gly Asn Asp Ala His Arg Phe Tyr
85 90 95

Asp Thr Leu Leu Arg Asn Leu Ser Asn Asp Thr Lys His Val Glu His
100 105 110

Val	Gln	Asp	Phe	Trp	Gly	Asp	Pro	Leu	Thr	Ala	Ala	Gly	Ser	Gln	Ser
		115				120						125			

Thr Asp Gly Lys Ala Ala Tyr Val Gln Val Tyr Leu Ala Gly Asn Gln
130 135 140

Gly Glu Ala Leu Ser Ile Glu Ser Val Asp Ala Val Arg Asp Ile Val
145 150 155 160

Ala His Thr Pro Pro Pro Ala Gly Val Lys Ala Tyr Val Thr Gly Ala
165 170 175

Ala Pro Leu Met Ala Asp Gln Phe Gln Val Gly Ser Lys Gly Thr Ala
180 185 190

Lys Val Thr Gly Ile Thr Leu Val Val Ile Ala Val Met Leu Leu Phe
195 200 205

Val Tyr Arg Ser Val Val Thr Met Val Leu Val Leu Ile Thr Val Leu
210 215 220

Ile Glu Leu Ala Ala Ala Arg Gly Ile Val Ala Phe Leu Gly Asn Ala
225 230 235 240

Gly Val Ile Gly Leu Ser Thr Tyr Ser Thr Asn Leu Leu Thr Leu Leu
245 250 255

Val Ile Ala Ala Gly Thr Asp Tyr Ala Ile Phe Val Leu Gly Arg Tyr
260 265 270

His Glu Ala Arg Tyr Ala Ala Gln Asp Arg Glu Thr Ala Phe Tyr Thr
275 280 285

Met Tyr Arg Gly Thr Ala His Val Val Leu Gly Ser Gly Leu Thr Val
290 295 300

Ala Gly Ala Val Tyr Cys Leu Ser Phe Thr Arg Leu Pro Tyr Phe Gln
305 310 315 320

Ser Leu Gly Ile Pro Ala Ser Ile Gly Val Met Ile Ala Leu Ala Ala
325 330 335

Ala Leu Ser Leu Ala Pro Ser Val Leu Ile Leu Gly Ser Arg Phe Gly
340 345 350

Cys Phe Glu Pro Lys Arg Arg Met Arg Thr Arg Gly Trp Arg Arg Ile
355 360 365

Gly Thr Ala Ile Val Arg Trp Pro Gly Pro Ile Leu Ala Val Ala Cys
370 375 380

Ala Ile Ala Val Val Gly Leu Leu Ala Leu Pro Gly Tyr Lys Thr Ser
385 390 395 400

Tyr Asp Ala Arg Tyr Tyr Met Pro Ala Thr Ala Pro Ala Asn Ile Gly
405 410 415

Tyr Met Ala Ala Glu Arg His Phe Pro Gln Ala Arg Leu Asn Pro Glu
420 425 430

Leu Leu Met Ile Glu Thr Asp His Asp Met Arg Asn Pro Ala Asp Met
435 440 445

Leu Ile Leu Asp Arg Ile Ala Lys Ala Val Phe His Leu Pro Gly Ile
450 455 460

Gly Leu Val Gln Ala Met Thr Arg Pro Leu Gly Thr Pro Ile Asp His
465 470 475 480

Ser Ser Ile Pro Phe Gln Ile Ser Met Gln Ser Val Gly Gln Ile Gln
485 490 495

Asn Leu Lys Tyr Gln Arg Asp Arg Ala Ala Asp Leu Leu Lys Gln Ala
500 505 510

Glu Glu Leu Gly Lys Thr Ile Glu Ile Leu Gln Arg Gln Tyr Ala Leu
515 520 525

Gln Gln Glu Leu Ala Ala Ala Thr His Glu Gln Ala Glu Ser Phe His
530 535 540

Gln Thr Ile Ala Thr Val Asn Glu Leu Arg Asp Arg Ile Ala Asn Phe
 545 550 555 560

Asp Asp Phe Phe Arg Pro Ile Arg Ser Tyr Phe Tyr Trp Glu Lys His
 565 570 575

Cys Tyr Asp Ile Pro Ser Cys Trp Ala Leu Arg Ser Val Phe Asp Thr
 580 585 590

Ile Asp Gly Ile Asp Gln Leu Gly Glu Gln Leu Ala Ser Val Thr Val
 595 600 605

Thr Leu Asp Lys Leu Ala Ala Ile Gln Pro Gln Leu Val Ala Leu Leu
 610 615 620

Pro Asp Glu Ile Ala Ser Gln Gln Ile Asn Arg Glu Leu Ala Leu Ala
 625 630 635 640

Asn Tyr Ala Thr Met Ser Gly Ile Tyr Ala Gln Thr Ala Ala Leu Ile
 645 650 655

Glu Asn Ala Ala Ala Met Gly Gln Ala Phe Asp Ala Ala Lys Asn Asp
 660 665 670

Asp Ser Phe Tyr Leu Pro Pro Glu Ala Phe Asp Asn Pro Asp Phe Gln
 675 680 685

Arg Gly Leu Lys Leu Phe Leu Ser Ala Asp Gly Lys Ala Ala Arg Met
 690 695 700

Ile Ile Ser His Glu Gly Asp Pro Ala Thr Pro Glu Gly Ile Ser His
 705 710 715 720

Ile Asp Ala Ile Lys Gln Ala Ala His Glu Ala Val Lys Gly Thr Pro
 725 730 735

Met Ala Gly Ala Gly Ile Tyr Leu Ala Gly Thr Ala Ala Thr Phe Lys
 740 745 750

Asp Ile Gln Asp Gly Ala Thr Tyr Asp Leu Leu Ile Ala Gly Ile Ala
 755 760 765

Ala Leu Ser Leu Ile Leu Leu Ile Met Met Ile Ile Thr Arg Ser Leu
 770 775 780

Val Ala Ala Leu Val Ile Val Gly Thr Val Ala Leu Ser Leu Gly Ala
 785 790 795 800

Ser Phe Gly Leu Ser Val Leu Val Trp Gln His Leu Leu Gly Ile Gln
 805 810 815

Leu Tyr Trp Ile Val Leu Ala Leu Ala Val Ile Leu Leu Leu Ala Val
 820 825 830

Gly Ser Asp Tyr Asn Leu Leu Leu Ile Ser Arg Phe Lys Glu Glu Ile
 835 840 845

Gly Ala Gly Leu Asn Thr Gly Ile Ile Arg Ala Met Ala Gly Thr Gly
 850 855 860

Gly Val Val Thr Ala Ala Gly Leu Val Phe Ala Ala Thr Met Ser Ser
 865 870 875 880

Phe Val Phe Ser Asp Leu Arg Val Leu Gly Gln Ile Gly Thr Thr Ile
 885 890 895

Gly Leu Gly Leu Leu Phe Asp Thr Leu Val Val Arg Ala Phe Met Thr
 900 905 910

Pro Ser Ile Ala Val Leu Leu Gly Arg Trp Phe Trp Trp Pro Gln Arg
 915 920 925

Val Arg Pro Arg Pro Ala Ser Arg Met Leu Arg Pro Tyr Gly Pro Arg
 930 935 940

Pro Val Val Arg Glu Leu Leu Leu Arg Glu Gly Asn Asp Asp Pro Arg
 945 950 955 960

Thr Gln Val Ala Thr His Arg
 965

<210> 3

<211> 148

<212> PRT

<213> Mycobacterium tuberculosis

<400> 3

Val Gln Gly Ile Ser Val Thr Gly Leu Val Lys Arg Gly Trp Met Val
 1 5 10 15

Leu Val Ala Val Ala Val Val Ala Val Ala Gly Phe Ser Val Tyr Arg
 20 25 30

Leu His Gly Ile Phe Gly Ser His Asp Thr Thr Ser Thr Ala Gly Gly
 35 40 45

Val Ala Asn Asp Ile Lys Pro Phe Asn Pro Lys Gln Val Thr Leu Glu
 50 55 60

Val Phe Gly Ala Pro Gly Thr Val Ala Thr Ile Asn Tyr Leu Asp Val
 65 70 75 80

Asp Ala Thr Pro Arg Gln Val Leu Asp Thr Thr Leu Pro Trp Ser Tyr
 85 90 95

Thr Ile Thr Thr Thr Leu Pro Ala Val Phe Ala Asn Val Val Ala Gln
 100 105 110

Gly Asp Ser Asn Ser Ile Gly Cys Arg Ile Thr Val Asn Gly Val Val
 115 120 125

Lys Asp Glu Arg Ile Val Asn Glu Val Arg Ala Tyr Thr Phe Cys Leu
 130 135 140

Asp Lys Ser Ser
 145

<210> 4

<211> 2153

<212> DNA

<213> Mycobacterium tuberculosis

<400> 4

ctggttgccg tggcgggtggt ggcggctcgc ggattcagcg tctatcggtt gcaaggcatc	60
ttcggtctgc acgacaccac ctgcaccgcc ggtggtgtcg cgaacgacat caagccgttc	120
aaccccaaac aggtaaccct cgaggtcttt ggcgctcccg gaaccgtggc aacgatcaat	180
tatctggacg tggatgccac acctcggcaa gtcttggaac cgaccctgcc gtgggtcatac	240
acgatcacga cgaccctgcc cgcgggtcttc gccaatgttg tcgcgcaagg cgacagcaat	300
tccatcggtt gccgcatcac cgtcaacggt gtagtcaagg acgaaaggat cgtcaacgaa	360

gtgcgcgcct	ataccttctg	cctcgacaag	tcctcatgag	caaccaccac	cgcccgcggc	420
cttggttgcc	gcacaccatc	cgacggcttt	cgttgccgat	cttgctgttt	tgggtgggtg	480
tggccgccat	aaccaatgcc	gccgtgccgc	aattggaggt	ggtcggggag	gcgcataacg	540
tcgcacagag	ctccccgat	gacccgtcgc	tgcaggcgat	gaaacgcata	ggcaagggtg	600
tccacgagtt	cgattccgac	agtgcggcca	tgatcgtctt	ggaaggcgat	aagccgctcg	660
gcaacgacgc	ccaccggttc	tacgacaccc	tgctccgcaa	cctttcaaac	gacaccaaac	720
acgtcgagca	cgttcaggac	ttctggggcg	atccgctgac	cgcgcccggc	tcgcaaagca	780
ccgacggcaa	agccgcctac	gttcagggtc	atctcgccgg	caaccaaggc	gaggcggttg	840
caatcgagtc	cgtcgacgcg	gtgcgcgaca	tcgtcgccca	tacgccacca	ccggccgggg	900
tcaaggccta	cgtcaccggc	gcggccccgc	tcattggcca	tcagtttcag	gtgggcagca	960
aaggaaccgc	gaaagttacc	gggataactc	tggttgatgat	cgcggtgatg	ttgctcttcg	1020
tataccgttc	cgtcgtcacc	atggctcctg	tgcttatcac	ggttcttatt	gagttggccg	1080
cgccccgcgg	gacgtcgtct	tttctcgga	acgcgggggt	aatcgggctg	tcgacatact	1140
cgacgaatct	gctcacacta	ttggtaatcg	cggcgggcac	agactacgcg	atTTTTgtcc	1200
tcggccgcta	tcacgaggcg	cgctacgccg	cacaggatcg	ggaaacggcc	ttctacacga	1260
tgtatcgccg	gaccgcccac	gtcgtcttgg	gctcggggtc	gaccgttgcc	ggcgcggtgt	1320
attgcctgag	ctttaccgcg	ctaccctatt	ttcaaagcct	gggtattccc	gcctcgatag	1380
gggtgatgat	tgcgttgcca	gccgcgtcca	gcctggcccc	atccgtgctc	atcttgggca	1440
gtcgtttcgg	ttgtttcgaa	cccaagcgca	ggatgaggac	caggggatgg	cggcgcatac	1500
gcacggccat	cgtgcgttgg	ccgggaccca	tcctggcagt	ggcgtgcgca	attgcggtgg	1560
tgggtctgct	cgcgctgccg	ggatacaaaa	cgagctacga	cgctcgctat	tacatgcccc	1620
ccaccgcccc	ggccaatatt	ggctacatgg	ccgcggagcg	acattttccc	caagcgcggc	1680
tgaatcccga	actactgatg	atcgagacgg	atcacgatat	gcgcaatccg	gccgacatgc	1740
tcattcttga	taggatcgcc	aaggctgtct	tccatctgcc	cggcataggg	ctggtgcagg	1800
ccatgaccgg	gccgctagga	accccgattg	accacagctc	gataccgttt	cagatcagca	1860
tgcaaagcgt	cggccagatt	cagaatctca	agtatcagag	ggaccgagca	gccgacttgc	1920
tgaagcaggc	cgaagagctg	gggaagacga	tcgaaatctt	gcagcgccaa	tatgccctac	1980
agcaggaact	cgcgggccgt	actcacgagc	aagccgaaag	ctttcaccaa	acgatcgcca	2040
cggtaaacga	actgcgagat	aggatcgcca	atttcgacga	tttcttcagg	ccgattcgta	2100

gttacttttta ctgggaaaag cactgctacg atatcccagag ctgctgggcg ctg 2153

<210> 5
 <211> 2904
 <212> DNA
 <213> Mycobacterium complex

<220>
 <221> CDS
 <222> (1)..(2901)

<400> 5
 atg agc aac cac cac cgc ccg cgg cct tgg ttg ccg cac acc atc cga 48
 Met Ser Asn His His Arg Pro Arg Pro Trp Leu Pro His Thr Ile Arg
 1 5 10 15

cgg ctt tcg ttg ccg atc ttg ctg ttt tgg gtg ggt gtg gcc gcc ata 96
 Arg Leu Ser Leu Pro Ile Leu Leu Phe Trp Val Gly Val Ala Ala Ile
 20 25 30

acc aat gcc gcc gtg ccg caa ttg gag gtg gtc ggg gag gcg cat aac 144
 Thr Asn Ala Ala Val Pro Gln Leu Glu Val Val Gly Glu Ala His Asn
 35 40 45

gtc gca cag agc tcc ccg gat gac ccg tcg ctg cag gcg atg aaa cgc 192
 Val Ala Gln Ser Ser Pro Asp Asp Pro Ser Leu Gln Ala Met Lys Arg
 50 55 60

atc ggc aag gtg ttc cac gag ttc gat tcc gac agt gcg gcc atg atc 240
 Ile Gly Lys Val Phe His Glu Phe Asp Ser Asp Ser Ala Ala Met Ile
 65 70 75 80

gtc ttg gaa ggc gat aag ccg ctc ggc aac gac gcc cac cgg ttc tac 288
 Val Leu Glu Gly Asp Lys Pro Leu Gly Asn Asp Ala His Arg Phe Tyr
 85 90 95

gac acc ctg ctc cgc aac ctt tca aac gac acc aaa cac gtc gag cac 336
 Asp Thr Leu Leu Arg Asn Leu Ser Asn Asp Thr Lys His Val Glu His
 100 105 110

gtt cag gac ttc tgg ggc gat ccg ctg acc gcg gcc ggc tcg caa agc 384
 Val Gln Asp Phe Trp Gly Asp Pro Leu Thr Ala Ala Gly Ser Gln Ser
 115 120 125

acc gac ggc aaa gcc gcc tac gtt cag gtc tat ctc gcc ggc aac caa 432
 Thr Asp Gly Lys Ala Ala Tyr Val Gln Val Tyr Leu Ala Gly Asn Gln
 130 135 140

ggc gag gcg ttg tca atc gag tcc gtc gac gcg gtg cgc gac atc gtc 480
 Gly Glu Ala Leu Ser Ile Glu Ser Val Asp Ala Val Arg Asp Ile Val
 145 150 155 160

gcc cat acg cca cca ccg gcc ggg gtc aag gcc tac gtc acc ggc gcg 528
 Ala His Thr Pro Pro Ala Gly Val Lys Ala Tyr Val Thr Gly Ala
 165 170 175

gcc ccg ctc atg gcc gat cag ttt cag gtg ggc agc aaa gga acc gcg Ala Pro Leu Met Ala Asp Gln Phe Gln Val Gly Ser Lys Gly Thr Ala 180 185 190	576
aaa gtt acc ggg ata act ctg gtt gtg atc gcg gtg atg ttg ctc ttc Lys Val Thr Gly Ile Thr Leu Val Val Ile Ala Val Met Leu Leu Phe 195 200 205	624
gta tac cgt tcc gtc gtc acc atg gtc ctg gtg ctt atc acg gtt ctt Val Tyr Arg Ser Val Val Thr Met Val Leu Val Leu Ile Thr Val Leu 210 215 220	672
att gag ttg gcc gcg gcc cgc ggg atc gtc gct ttt ctc gga aac gcc Ile Glu Leu Ala Ala Ala Arg Gly Ile Val Ala Phe Leu Gly Asn Ala 225 230 235 240	720
ggg gta atc ggg ctg tcg aca tac tcg acg aat ctg ctc aca cta ttg Gly Val Ile Gly Leu Ser Thr Tyr Ser Thr Asn Leu Leu Thr Leu Leu 245 250 255	768
gta atc gcg gcg ggc aca gac tac gcg att ttt gtc ctc ggc cgc tat Val Ile Ala Ala Gly Thr Asp Tyr Ala Ile Phe Val Leu Gly Arg Tyr 260 265 270	816
cac gag gcg cgc tac gcc gca cag gat cgg gaa acg gcc ttc tac acg His Glu Ala Arg Tyr Ala Ala Gln Asp Arg Glu Thr Ala Phe Tyr Thr 275 280 285	864
atg tat cgc ggg acc gcc cac gtc gtc ttg ggc tcg ggt ctg acc gtt Met Tyr Arg Gly Thr Ala His Val Val Leu Gly Ser Gly Leu Thr Val 290 295 300	912
gcc ggc gcg gtg tat tgc ctg agc ttt acc cgg cta ccc tat ttt caa Ala Gly Ala Val Tyr Cys Leu Ser Phe Thr Arg Leu Pro Tyr Phe Gln 305 310 315 320	960
agc ctg ggt att ccc gcc tcg ata ggg gtg atg att gcg ttg gca gcc Ser Leu Gly Ile Pro Ala Ser Ile Gly Val Met Ile Ala Leu Ala Ala 325 330 335	1008
gcg ctc agc ctg gcc cca tcc gtg ctc atc ttg ggc agt cgt ttc ggt Ala Leu Ser Leu Ala Pro Ser Val Leu Ile Leu Gly Ser Arg Phe Gly 340 345 350	1056
tgt ttc gaa ccc aag cgc agg atg agg acc agg gga tgg cgg cgc atc Cys Phe Glu Pro Lys Arg Arg Met Arg Thr Arg Gly Trp Arg Arg Ile 355 360 365	1104
ggc acg gcc atc gtg cgt tgg ccg gga ccc atc ctg gca gtg gcg tgc Gly Thr Ala Ile Val Arg Trp Pro Gly Pro Ile Leu Ala Val Ala Cys 370 375 380	1152
gca att gcg gtg gtg ggt ctg ctc gcg ctg ccg gga tac aaa acg agc Ala Ile Ala Val Val Gly Leu Leu Ala Leu Pro Gly Tyr Lys Thr Ser 385 390 395 400	1200

tac gac gct cgc tat tac atg ccc gcc acc gcc ccg gcc aat att ggc Tyr Asp Ala Arg Tyr Tyr Met Pro Ala Thr Ala Pro Ala Asn Ile Gly 405 410 415	1248
tac atg gcc gcg gag cga cat ttt ccc caa gcg cgg ctg aat ccc gaa Tyr Met Ala Ala Glu Arg His Phe Pro Gln Ala Arg Leu Asn Pro Glu 420 425 430	1296
cta ctg atg atc gag acg gat cac gat atg cgc aat ccg gcc gac atg Leu Leu Met Ile Glu Thr Asp His Asp Met Arg Asn Pro Ala Asp Met 435 440 445	1344
ctc atc ttg gat agg atc gcc aag gct gtc ttc cat ctg ccc ggc ata Leu Ile Leu Asp Arg Ile Ala Lys Ala Val Phe His Leu Pro Gly Ile 450 455 460	1392
ggg ctg gtg cag gcc atg acc cgg ccg cta gga acc ccg att gac cac Gly Leu Val Gln Ala Met Thr Arg Pro Leu Gly Thr Pro Ile Asp His 465 470 475 480	1440
agc tcg ata ccg ttt cag atc agc atg caa agc gtc ggc cag att cag Ser Ser Ile Pro Phe Gln Ile Ser Met Gln Ser Val Gly Gln Ile Gln 485 490 495	1488
aat ctc aag tat cag agg gac cga gca gcc gac ttg ctg aag cag gcc Asn Leu Lys Tyr Gln Arg Asp Arg Ala Ala Asp Leu Leu Lys Gln Ala 500 505 510	1536
gaa gag ctg ggg aag acg atc gaa atc ttg cag cgc caa tat gcc cta Glu Glu Leu Gly Lys Thr Ile Glu Ile Leu Gln Arg Gln Tyr Ala Leu 515 520 525	1584
cag cag gaa ctc gcg gcc gct act cac gag caa gcc gaa agc ttt cac Gln Gln Glu Leu Ala Ala Ala Thr His Glu Gln Ala Glu Ser Phe His 530 535 540	1632
caa acg atc gcc acg gta aag gaa ctg cga gat agg atc gcc aat ttc Gln Thr Ile Ala Thr Val Lys Glu Leu Arg Asp Arg Ile Ala Asn Phe 545 550 555 560	1680
gac gat ttc ttc agg ccg att cgt agt tac ttt tac tgg gaa aag cac Asp Asp Phe Phe Arg Pro Ile Arg Ser Tyr Phe Tyr Trp Glu Lys His 565 570 575	1728
tgc tac gat atc ccg agc tgc tgg gcg ctg aga tcc gtc ttt gac acg Cys Tyr Asp Ile Pro Ser Cys Trp Ala Leu Arg Ser Val Phe Asp Thr 580 585 590	1776
atc gac ggt atc gac caa ctc ggc gag cag ctg gcc agc gtg acc gta Ile Asp Gly Ile Asp Gln Leu Gly Glu Gln Leu Ala Ser Val Thr Val 595 600 605	1824
acc ttg gac aag ttg gct gcg atc cag cct caa ttg gtg gcg ctg cta Thr Leu Asp Lys Leu Ala Ala Ile Gln Pro Gln Leu Val Ala Leu Leu 610 615 620	1872

cca gac gag atc gcc agc cag cag atc aat cgg gaa ctg gcg ctg gct Pro Asp Glu Ile Ala Ser Gln Gln Ile Asn Arg Glu Leu Ala Leu Ala 625 630 635 640	1920
aac tac gcc acc atg tcc ggg atc tat gcc cag acg gcg gcc ttg atc Asn Tyr Ala Thr Met Ser Gly Ile Tyr Ala Gln Thr Ala Ala Leu Ile 645 650 655	1968
gaa aac gct gcc gcc atg gga caa gcc ttt gac gcc gcc aag aac gac Glu Asn Ala Ala Ala Met Gly Gln Ala Phe Asp Ala Ala Lys Asn Asp 660 665 670	2016
gac tcc ttc tat ctg ccg ccg gag gct ttt gac aac cca gat ttc cag Asp Ser Phe Tyr Leu Pro Pro Glu Ala Phe Asp Asn Pro Asp Phe Gln 675 680 685	2064
cgc ggc ctg aaa ttg ttc ctg tcg gca gac ggt aag gcg gct cgg atg Arg Gly Leu Lys Leu Phe Leu Ser Ala Asp Gly Lys Ala Ala Arg Met 690 695 700	2112
atc atc tcc cat gaa ggc gat ccc gcc acc ccc gaa ggc att tcg cat Ile Ile Ser His Glu Gly Asp Pro Ala Thr Pro Glu Gly Ile Ser His 705 710 715 720	2160
atc gac gcg atc aag cag gcg gcc cac gag gcc gtg aag ggc act ccc Ile Asp Ala Ile Lys Gln Ala Ala His Glu Ala Val Lys Gly Thr Pro 725 730 735	2208
atg gcg ggt gct ggg atc tat ctg gcc ggc acg gcc gcc acc ttc aag Met Ala Gly Ala Gly Ile Tyr Leu Ala Gly Thr Ala Ala Thr Phe Lys 740 745 750	2256
gac att caa gac ggc gcc acc tac gac ctc ctg atc gcc gga ata gcc Asp Ile Gln Asp Gly Ala Thr Tyr Asp Leu Leu Ile Ala Gly Ile Ala 755 760 765	2304
gcg ctg agc ttg att ttg ctc atc atg atg atc att acc cga agc ctg Ala Leu Ser Leu Ile Leu Leu Ile Met Met Ile Ile Thr Arg Ser Leu 770 775 780	2352
gtt gcg gcg ctg gtg atc gtg ggc acg gtg gcg ctg tcg ttg ggc gct Val Ala Ala Leu Val Ile Val Gly Thr Val Ala Leu Ser Leu Gly Ala 785 790 795 800	2400
tct ttt ggc ctg tcc gtg ctg gtg tgg cag cat ctt ctc ggt atc cag Ser Phe Gly Leu Ser Val Leu Val Trp Gln His Leu Leu Gly Ile Gln 805 810 815	2448
ttg tac tgg atc gtg ctc gcg ctg gcc gtc atc ctg ctc ctg gcc gtg Leu Tyr Trp Ile Val Leu Ala Leu Ala Val Ile Leu Leu Leu Ala Val 820 825 830	2496
gga tcg gac tat aac ttg ctg ctg att tcc cga ttc aag gag gag atc Gly Ser Asp Tyr Asn Leu Leu Leu Ile Ser Arg Phe Lys Glu Glu Ile 835 840 845	2544

ggt gca ggt ttg aac acc ggc atc atc cgt gcg atg gcc ggc acc ggc 2592
 Gly Ala Gly Leu Asn Thr Gly Ile Ile Arg Ala Met Ala Gly Thr Gly
 850 855 860

ggg gtg gtg acc gct gcc ggc ctg gtg ttc gcc gcc act atg tct tcg 2640
 Gly Val Val Thr Ala Ala Gly Leu Val Phe Ala Ala Thr Met Ser Ser
 865 870 875 880

ttc gtg ttc agt gat ttg cgg gtc ctc ggt cag atc ggg acc acc att 2688
 Phe Val Phe Ser Asp Leu Arg Val Leu Gly Gln Ile Gly Thr Thr Ile
 885 890 895

ggt ctt ggg ctg ctg ttc gac acg ctg gtg gtg cgc gcg ttc atg acc 2736
 Gly Leu Gly Leu Leu Phe Asp Thr Leu Val Val Arg Ala Phe Met Thr
 900 905 910

ccg tcc atc gcg gtg ctg ctc ggg cgc tgg ttc tgg tgg ccg caa cga 2784
 Pro Ser Ile Ala Val Leu Leu Gly Arg Trp Phe Trp Trp Pro Gln Arg
 915 920 925

gtg cgc ccg cgc cct gcc agc agg atg ctt cgg ccg tac ggc ccg ccg 2832
 Val Arg Pro Arg Pro Ala Ser Arg Met Leu Arg Pro Tyr Gly Pro Arg
 930 935 940

ccc gtg gtt cgt gaa ttg ctg ctg cgc gag ggc aac gat gac ccg aga 2880
 Pro Val Val Arg Glu Leu Leu Leu Arg Glu Gly Asn Asp Asp Pro Arg
 945 950 955 960

act cag gtg gct acc cac cgt taa 2904
 Thr Gln Val Ala Thr His Arg
 965

<210> 6
 <211> 967
 <212> PRT
 <213> Mycobacterium complex

<400> 6
 Met Ser Asn His His Arg Pro Arg Pro Trp Leu Pro His Thr Ile Arg
 1 5 10 15

Arg Leu Ser Leu Pro Ile Leu Leu Phe Trp Val Gly Val Ala Ala Ile
 20 25 30

Thr Asn Ala Ala Val Pro Gln Leu Glu Val Val Gly Glu Ala His Asn
 35 40 45

Val Ala Gln Ser Ser Pro Asp Asp Pro Ser Leu Gln Ala Met Lys Arg
 50 55 60

Ile Gly Lys Val Phe His Glu Phe Asp Ser Asp Ser Ala Ala Met Ile
 65 70 75 80

Val	Leu	Glu	Gly	Asp 85	Lys	Pro	Leu	Gly	Asn 90	Asp	Ala	His	Arg	Phe 95	Tyr
Asp	Thr	Leu	Leu 100	Arg	Asn	Leu	Ser	Asn 105	Asp	Thr	Lys	His	Val 110	Glu	His
Val	Gln	Asp 115	Phe	Trp	Gly	Asp	Pro 120	Leu	Thr	Ala	Ala	Gly 125	Ser	Gln	Ser
Thr	Asp 130	Gly	Lys	Ala	Ala	Tyr 135	Val	Gln	Val	Tyr	Leu 140	Ala	Gly	Asn	Gln
Gly 145	Glu	Ala	Leu	Ser	Ile 150	Glu	Ser	Val	Asp	Ala 155	Val	Arg	Asp	Ile 160	Val
Ala	His	Thr	Pro	Pro 165	Pro	Ala	Gly	Val	Lys 170	Ala	Tyr	Val	Thr	Gly 175	Ala
Ala	Pro	Leu	Met 180	Ala	Asp	Gln	Phe	Gln 185	Val	Gly	Ser	Lys	Gly 190	Thr	Ala
Lys	Val	Thr 195	Gly	Ile	Thr	Leu	Val 200	Val	Ile	Ala	Val	Met 205	Leu	Leu	Phe
Val	Tyr 210	Arg	Ser	Val	Val	Thr 215	Met	Val	Leu	Val	Leu 220	Ile	Thr	Val	Leu
Ile 225	Glu	Leu	Ala	Ala	Ala 230	Arg	Gly	Ile	Val	Ala 235	Phe	Leu	Gly	Asn 240	Ala
Gly	Val	Ile	Gly	Leu 245	Ser	Thr	Tyr	Ser	Thr 250	Asn	Leu	Leu	Thr	Leu 255	Leu
Val	Ile	Ala	Ala 260	Gly	Thr	Asp	Tyr	Ala 265	Ile	Phe	Val	Leu	Gly 270	Arg	Tyr
His	Glu	Ala 275	Arg	Tyr	Ala	Ala	Gln 280	Asp	Arg	Glu	Thr	Ala 285	Phe	Tyr	Thr
Met	Tyr 290	Arg	Gly	Thr	Ala	His 295	Val	Val	Leu	Gly	Ser 300	Gly	Leu	Thr	Val

Ala Gly Ala Val Tyr Cys Leu Ser Phe Thr Arg Leu Pro Tyr Phe Gln
305 310 315 320

Ser Leu Gly Ile Pro Ala Ser Ile Gly Val Met Ile Ala Leu Ala Ala
325 330 335

Ala Leu Ser Leu Ala Pro Ser Val Leu Ile Leu Gly Ser Arg Phe Gly
340 345 350

Cys Phe Glu Pro Lys Arg Arg Met Arg Thr Arg Gly Trp Arg Arg Ile
355 360 365

Gly Thr Ala Ile Val Arg Trp Pro Gly Pro Ile Leu Ala Val Ala Cys
370 375 380

Ala Ile Ala Val Val Gly Leu Leu Ala Leu Pro Gly Tyr Lys Thr Ser
385 390 395 400

Tyr Asp Ala Arg Tyr Tyr Met Pro Ala Thr Ala Pro Ala Asn Ile Gly
405 410 415

Tyr Met Ala Ala Glu Arg His Phe Pro Gln Ala Arg Leu Asn Pro Glu
420 425 430

Leu Leu Met Ile Glu Thr Asp His Asp Met Arg Asn Pro Ala Asp Met
435 440 445

Leu Ile Leu Asp Arg Ile Ala Lys Ala Val Phe His Leu Pro Gly Ile
450 455 460

Gly Leu Val Gln Ala Met Thr Arg Pro Leu Gly Thr Pro Ile Asp His
465 470 475 480

Ser Ser Ile Pro Phe Gln Ile Ser Met Gln Ser Val Gly Gln Ile Gln
485 490 495

Asn Leu Lys Tyr Gln Arg Asp Arg Ala Ala Asp Leu Leu Lys Gln Ala
500 505 510

Glu Glu Leu Gly Lys Thr Ile Glu Ile Leu Gln Arg Gln Tyr Ala Leu
515 520 525

Gln Gln Glu Leu Ala Ala Ala Thr His Glu Gln Ala Glu Ser Phe His
530 535 540

Gln Thr Ile Ala Thr Val Lys Glu Leu Arg Asp Arg Ile Ala Asn Phe
 545 550 555 560

Asp Asp Phe Phe Arg Pro Ile Arg Ser Tyr Phe Tyr Trp Glu Lys His
 565 570 575

Cys Tyr Asp Ile Pro Ser Cys Trp Ala Leu Arg Ser Val Phe Asp Thr
 580 585 590

Ile Asp Gly Ile Asp Gln Leu Gly Glu Gln Leu Ala Ser Val Thr Val
 595 600 605

Thr Leu Asp Lys Leu Ala Ala Ile Gln Pro Gln Leu Val Ala Leu Leu
 610 615 620

Pro Asp Glu Ile Ala Ser Gln Gln Ile Asn Arg Glu Leu Ala Leu Ala
 625 630 635 640

Asn Tyr Ala Thr Met Ser Gly Ile Tyr Ala Gln Thr Ala Ala Leu Ile
 645 650 655

Glu Asn Ala Ala Ala Met Gly Gln Ala Phe Asp Ala Ala Lys Asn Asp
 660 665 670

Asp Ser Phe Tyr Leu Pro Pro Glu Ala Phe Asp Asn Pro Asp Phe Gln
 675 680 685

Arg Gly Leu Lys Leu Phe Leu Ser Ala Asp Gly Lys Ala Ala Arg Met
 690 695 700

Ile Ile Ser His Glu Gly Asp Pro Ala Thr Pro Glu Gly Ile Ser His
 705 710 715 720

Ile Asp Ala Ile Lys Gln Ala Ala His Glu Ala Val Lys Gly Thr Pro
 725 730 735

Met Ala Gly Ala Gly Ile Tyr Leu Ala Gly Thr Ala Ala Thr Phe Lys
 740 745 750

Asp Ile Gln Asp Gly Ala Thr Tyr Asp Leu Leu Ile Ala Gly Ile Ala
 755 760 765

Ala Leu Ser Leu Ile Leu Leu Ile Met Met Ile Ile Thr Arg Ser Leu
770 775 780

Val Ala Ala Leu Val Ile Val Gly Thr Val Ala Leu Ser Leu Gly Ala
785 790 795 800

Ser Phe Gly Leu Ser Val Leu Val Trp Gln His Leu Leu Gly Ile Gln
805 810 815

Leu Tyr Trp Ile Val Leu Ala Leu Ala Val Ile Leu Leu Leu Ala Val
820 825 830

Gly Ser Asp Tyr Asn Leu Leu Leu Ile Ser Arg Phe Lys Glu Glu Ile
835 840 845

Gly Ala Gly Leu Asn Thr Gly Ile Ile Arg Ala Met Ala Gly Thr Gly
850 855 860

Gly Val Val Thr Ala Ala Gly Leu Val Phe Ala Ala Thr Met Ser Ser
865 870 875 880

Phe Val Phe Ser Asp Leu Arg Val Leu Gly Gln Ile Gly Thr Thr Ile
885 890 895

Gly Leu Gly Leu Leu Phe Asp Thr Leu Val Val Arg Ala Phe Met Thr
900 905 910

Pro Ser Ile Ala Val Leu Leu Gly Arg Trp Phe Trp Trp Pro Gln Arg
915 920 925

Val Arg Pro Arg Pro Ala Ser Arg Met Leu Arg Pro Tyr Gly Pro Arg
930 935 940

Pro Val Val Arg Glu Leu Leu Leu Arg Glu Gly Asn Asp Asp Pro Arg
945 950 955 960

Thr Gln Val Ala Thr His Arg
965

<210> 7

<211> 1758

<212> DNA

<213> Mycobacterium complex

<220>

<221> CDS

<222> (1)..(1758)

<400> 7

atg agc aac cac cac cgc ccg cgg cct tgg ttg ccg cac acc atc cga	48
Met Ser Asn His His Arg Pro Arg Pro Trp Leu Pro His Thr Ile Arg	
1 5 10 15	
cgg ctt tcg ttg ccg atc ttg ctg ttt tgg gtg ggt gtg gcc gcc ata	96
Arg Leu Ser Leu Pro Ile Leu Leu Phe Trp Val Gly Val Ala Ala Ile	
20 25 30	
acc aat gcc gcc gtg ccg caa ttg gag gtg gtc ggg gag gcg cat aac	144
Thr Asn Ala Ala Val Pro Gln Leu Glu Val Val Gly Glu Ala His Asn	
35 40 45	
gtc gca cag agc tcc ccg gat gac ccg tcg ctg cag gcg atg aaa cgc	192
Val Ala Gln Ser Ser Pro Asp Asp Pro Ser Leu Gln Ala Met Lys Arg	
50 55 60	
atc ggc aag gtg ttc cac gag ttc gat tcc gac agt gcg gcc atg atc	240
Ile Gly Lys Val Phe His Glu Phe Asp Ser Asp Ser Ala Ala Met Ile	
65 70 75 80	
gtc ttg gaa ggc gat aag ccg ctc ggc aac gac gcc cac cgg ttc tac	288
Val Leu Glu Gly Asp Lys Pro Leu Gly Asn Asp Ala His Arg Phe Tyr	
85 90 95	
gac acc ctg ctc cgc aac ctt tca aac gac acc aaa cac gtc gag cac	336
Asp Thr Leu Leu Arg Asn Leu Ser Asn Asp Thr Lys His Val Glu His	
100 105 110	
gtt cag gac ttc tgg ggc gat ccg ctg acc gcg gcc gcc tcg caa agc	384
Val Gln Asp Phe Trp Gly Asp Pro Leu Thr Ala Ala Gly Ser Gln Ser	
115 120 125	
acc gac ggc aaa gcc gcc tac gtt cag gtc tat ctc gcc gcc aac caa	432
Thr Asp Gly Lys Ala Ala Tyr Val Gln Val Tyr Leu Ala Gly Asn Gln	
130 135 140	
ggc gag gcg ttg tca atc gag tcc gtc gac gcg gtg cgc gac atc gtc	480
Gly Glu Ala Leu Ser Ile Glu Ser Val Asp Ala Val Arg Asp Ile Val	
145 150 155 160	
gcc cat acg cca cca ccg gcc ggg gtc aag gcc tac gtc acc gcc gcg	528
Ala His Thr Pro Pro Pro Ala Gly Val Lys Ala Tyr Val Thr Gly Ala	
165 170 175	
gcc ccg ctc atg gcc gat cag ttt cag gtg ggc agc aaa gga acc gcg	576
Ala Pro Leu Met Ala Asp Gln Phe Gln Val Gly Ser Lys Gly Thr Ala	
180 185 190	
aaa gtt acc ggg ata act ctg gtt gtg atc gcg gtg atg ttg ctc ttc	624
Lys Val Thr Gly Ile Thr Leu Val Val Ile Ala Val Met Leu Leu Phe	
195 200 205	

gta tac cgt tcc gtc gtc acc atg gtc ctg gtg ctt atc acg gtt ctt Val Tyr Arg Ser Val Val Thr Met Val Leu Val Leu Ile Thr Val Leu 210 215 220	672
att gag ttg gcc gcg gcc cgc ggg atc gtc gct ttt ctc gga aac gcc Ile Glu Leu Ala Ala Ala Arg Gly Ile Val Ala Phe Leu Gly Asn Ala 225 230 235 240	720
ggg gta atc ggg ctg tcg aca tac tcg acg aat ctg ctc aca cta ttg Gly Val Ile Gly Leu Ser Thr Tyr Ser Thr Asn Leu Leu Thr Leu Leu 245 250 255	768
gta atc gcg gcg ggc aca gac tac gcg att ttt gtc ctc ggc cgc tat Val Ile Ala Ala Gly Thr Asp Tyr Ala Ile Phe Val Leu Gly Arg Tyr 260 265 270	816
cac gag gcg cgc tac gcc gca cag gat cgg gaa acg gcc ttc tac acg His Glu Ala Arg Tyr Ala Ala Gln Asp Arg Glu Thr Ala Phe Tyr Thr 275 280 285	864
atg tat cgc ggg acc gcc cac gtc gtc ttg ggc tcg ggt ctg acc gtt Met Tyr Arg Gly Thr Ala His Val Val Leu Gly Ser Gly Leu Thr Val 290 295 300	912
gcc ggc gcg gtg tat tgc ctg agc ttt acc cgg cta ccc tat ttt caa Ala Gly Ala Val Tyr Cys Leu Ser Phe Thr Arg Leu Pro Tyr Phe Gln 305 310 315 320	960
agc ctg ggt att ccc gcc tcg ata ggg gtg atg att gcg ttg gca gcc Ser Leu Gly Ile Pro Ala Ser Ile Gly Val Met Ile Ala Leu Ala Ala 325 330 335	1008
gcg ctc agc ctg gcc cca tcc gtg ctc atc ttg ggc agt cgt ttc ggt Ala Leu Ser Leu Ala Pro Ser Val Leu Ile Leu Gly Ser Arg Phe Gly 340 345 350	1056
tgt ttc gaa ccc aag cgc agg atg agg acc agg gga tgg cgg cgc atc Cys Phe Glu Pro Lys Arg Arg Met Arg Thr Arg Gly Trp Arg Arg Ile 355 360 365	1104
ggc acg gcc atc gtg cgt tgg ccg gga ccc atc ctg gca gtg gcg tgc Gly Thr Ala Ile Val Arg Trp Pro Gly Pro Ile Leu Ala Val Ala Cys 370 375 380	1152
gca att gcg gtg gtg ggt ctg ctc gcg ctg ccg gga tac aaa acg agc Ala Ile Ala Val Val Gly Leu Leu Ala Leu Pro Gly Tyr Lys Thr Ser 385 390 395 400	1200
tac gac gct cgc tat tac atg ccc gcc acc gcc ccg gcc aat att ggc Tyr Asp Ala Arg Tyr Tyr Met Pro Ala Thr Ala Pro Ala Asn Ile Gly 405 410 415	1248
tac atg gcc gcg gag cga cat ttt ccc caa gcg cgg ctg aat ccc gaa Tyr Met Ala Ala Glu Arg His Phe Pro Gln Ala Arg Leu Asn Pro Glu 420 425 430	1296

cta ctg atg atc gag acg gat cac gat atg cgc aat ccg gcc gac atg 1344
 Leu Leu Met Ile Glu Thr Asp His Asp Met Arg Asn Pro Ala Asp Met
 435 440 445

ctc atc ttg gat agg atc gcc aag gct gtc ttc cat ctg ccc ggc ata 1392
 Leu Ile Leu Asp Arg Ile Ala Lys Ala Val Phe His Leu Pro Gly Ile
 450 455 460

ggg ctg gtg cag gcc atg acc cgg ccg cta gga acc ccg att gac cac 1440
 Gly Leu Val Gln Ala Met Thr Arg Pro Leu Gly Thr Pro Ile Asp His
 465 470 475 480

agc tcg ata ccg ttt cag atc agc atg caa agc gtc ggc cag att cag 1488
 Ser Ser Ile Pro Phe Gln Ile Ser Met Gln Ser Val Gly Gln Ile Gln
 485 490 495

aat ctc aag tat cag agg gac cga gca gcc gac ttg ctg aag cag gcc 1536
 Asn Leu Lys Tyr Gln Arg Asp Arg Ala Ala Asp Leu Leu Lys Gln Ala
 500 505 510

gaa gag ctg ggg aag acg atc gaa atc ttg cag cgc caa tat gcc cta 1584
 Glu Glu Leu Gly Lys Thr Ile Glu Ile Leu Gln Arg Gln Tyr Ala Leu
 515 520 525

cag cag gaa ctc gcg gcc gct act cac gag caa gcc gaa agc ttt cac 1632
 Gln Gln Glu Leu Ala Ala Thr His Glu Gln Ala Glu Ser Phe His
 530 535 540

caa acg atc gcc acg gta aag gaa ctg cga gat agg atc gcc aat ttc 1680
 Gln Thr Ile Ala Thr Val Lys Glu Leu Arg Asp Arg Ile Ala Asn Phe
 545 550 555 560

gac gat ttc ttc agg ccg att cgt agt tac ttt tac tgg gaa aag cac 1728
 Asp Asp Phe Phe Arg Pro Ile Arg Ser Tyr Phe Tyr Trp Glu Lys His
 565 570 575

tgc tac gat atc ccg agc tgc tgg gcg ctg 1758
 Cys Tyr Asp Ile Pro Ser Cys Trp Ala Leu
 580 585

<210> 8

<211> 586

<212> PRT

<213> Mycobacterium complex

<400> 8

Met Ser Asn His His Arg Pro Arg Pro Trp Leu Pro His Thr Ile Arg
 1 5 10 15

Arg Leu Ser Leu Pro Ile Leu Leu Phe Trp Val Gly Val Ala Ala Ile
 20 25 30

Thr Asn Ala Ala Val Pro Gln Leu Glu Val Val Gly Glu Ala His Asn
 35 40 45

Val Ala Gln Ser Ser Pro Asp Asp Pro Ser Leu Gln Ala Met Lys Arg
 50 55 60

Ile Gly Lys Val Phe His Glu Phe Asp Ser Asp Ser Ala Ala Met Ile
 65 70 75 80

Val Leu Glu Gly Asp Lys Pro Leu Gly Asn Asp Ala His Arg Phe Tyr
 85 90 95

Asp Thr Leu Leu Arg Asn Leu Ser Asn Asp Thr Lys His Val Glu His
 100 105 110

Val Gln Asp Phe Trp Gly Asp Pro Leu Thr Ala Ala Gly Ser Gln Ser
 115 120 125

Thr Asp Gly Lys Ala Ala Tyr Val Gln Val Tyr Leu Ala Gly Asn Gln
 130 135 140

Gly Glu Ala Leu Ser Ile Glu Ser Val Asp Ala Val Arg Asp Ile Val
 145 150 155 160

Ala His Thr Pro Pro Pro Ala Gly Val Lys Ala Tyr Val Thr Gly Ala
 165 170 175

Ala Pro Leu Met Ala Asp Gln Phe Gln Val Gly Ser Lys Gly Thr Ala
 180 185 190

Lys Val Thr Gly Ile Thr Leu Val Val Ile Ala Val Met Leu Leu Phe
 195 200 205

Val Tyr Arg Ser Val Val Thr Met Val Leu Val Leu Ile Thr Val Leu
 210 215 220

Ile Glu Leu Ala Ala Ala Arg Gly Ile Val Ala Phe Leu Gly Asn Ala
 225 230 235 240

Gly Val Ile Gly Leu Ser Thr Tyr Ser Thr Asn Leu Leu Thr Leu Leu
 245 250 255

Val Ile Ala Ala Gly Thr Asp Tyr Ala Ile Phe Val Leu Gly Arg Tyr
 260 265 270

His Glu Ala Arg Tyr Ala Ala Gln Asp Arg Glu Thr Ala Phe Tyr Thr
 275 280 285

Met Tyr Arg Gly Thr Ala His Val Val Leu Gly Ser Gly Leu Thr Val
 290 295 300

Ala Gly Ala Val Tyr Cys Leu Ser Phe Thr Arg Leu Pro Tyr Phe Gln
 305 310 315 320

Ser Leu Gly Ile Pro Ala Ser Ile Gly Val Met Ile Ala Leu Ala Ala
 325 330 335

Ala Leu Ser Leu Ala Pro Ser Val Leu Ile Leu Gly Ser Arg Phe Gly
 340 345 350

Cys Phe Glu Pro Lys Arg Arg Met Arg Thr Arg Gly Trp Arg Arg Ile
 355 360 365

Gly Thr Ala Ile Val Arg Trp Pro Gly Pro Ile Leu Ala Val Ala Cys
 370 375 380

Ala Ile Ala Val Val Gly Leu Leu Ala Leu Pro Gly Tyr Lys Thr Ser
 385 390 395 400

Tyr Asp Ala Arg Tyr Tyr Met Pro Ala Thr Ala Pro Ala Asn Ile Gly
 405 410 415

Tyr Met Ala Ala Glu Arg His Phe Pro Gln Ala Arg Leu Asn Pro Glu
 420 425 430

Leu Leu Met Ile Glu Thr Asp His Asp Met Arg Asn Pro Ala Asp Met
 435 440 445

Leu Ile Leu Asp Arg Ile Ala Lys Ala Val Phe His Leu Pro Gly Ile
 450 455 460

Gly Leu Val Gln Ala Met Thr Arg Pro Leu Gly Thr Pro Ile Asp His
 465 470 475 480

Ser Ser Ile Pro Phe Gln Ile Ser Met Gln Ser Val Gly Gln Ile Gln
 485 490 495

Asn Leu Lys Tyr Gln Arg Asp Arg Ala Ala Asp Leu Leu Lys Gln Ala
 500 505 510

Glu Glu Leu Gly Lys Thr Ile Glu Ile Leu Gln Arg Gln Tyr Ala Leu
 515 520 525

Gln Gln Glu Leu Ala Ala Ala Thr His Glu Gln Ala Glu Ser Phe His
 530 535 540

Gln Thr Ile Ala Thr Val Lys Glu Leu Arg Asp Arg Ile Ala Asn Phe
 545 550 555 560

Asp Asp Phe Phe Arg Pro Ile Arg Ser Tyr Phe Tyr Trp Glu Lys His
 565 570 575

Cys Tyr Asp Ile Pro Ser Cys Trp Ala Leu
 580 585

<210> 9

<211> 447

<212> DNA

<213> Mycobacterium complex

<220>

<221> CDS

<222> (1)..(444)

<400> 9

gtg	cag	ggg	att	tca	gtg	act	ggc	ctg	gtc	aaa	cgc	ggc	tgg	atg	gtg	48
Val	Gln	Gly	Ile	Ser	Val	Thr	Gly	Leu	Val	Lys	Arg	Gly	Trp	Met	Val	
1				5					10					15		

ctg	gtt	gcc	gtg	gcg	gtg	gtg	gcg	gtc	gcg	gga	ttc	agc	gtc	tat	cgg	96
Leu	Val	Ala	Val	Ala	Val	Val	Ala	Val	Ala	Gly	Phe	Ser	Val	Tyr	Arg	
			20					25					30			

ttg	cac	ggc	atc	ttc	ggc	tcg	cac	gac	acc	acc	tcg	acc	gcc	ggg	ggg	144
Leu	His	Gly	Ile	Phe	Gly	Ser	His	Asp	Thr	Thr	Ser	Thr	Ala	Gly	Gly	
		35					40					45				

gtc	gcg	aac	gac	atc	aag	ccg	ttc	aac	ccc	aaa	cag	gta	acc	ctc	gag	192
Val	Ala	Asn	Asp	Ile	Lys	Pro	Phe	Asn	Pro	Lys	Gln	Val	Thr	Leu	Glu	
		50				55					60					

gtc	ttt	ggc	gct	ccc	gga	acc	gtg	gca	acg	atc	aat	tat	ctg	gac	gtg	240
Val	Phe	Gly	Ala	Pro	Gly	Thr	Val	Ala	Thr	Ile	Asn	Tyr	Leu	Asp	Val	
65					70					75					80	

gat	gcc	aca	cct	cgg	caa	gtc	ctg	gac	acg	acc	ctg	ccg	tgg	tca	tac	288
Asp	Ala	Thr	Pro	Arg	Gln	Val	Leu	Asp	Thr	Thr	Leu	Pro	Trp	Ser	Tyr	
				85				90						95		

acg atc acg acg acc ctg ccc gcg gtc ttc gcc aat gtt gtc gcg caa 336
 Thr Ile Thr Thr Thr Leu Pro Ala Val Phe Ala Asn Val Val Ala Gln
 100 105 110

ggc gac agc aat tcc atc ggc tgc cgc atc acc gtc aac ggt gta gtc 384
 Gly Asp Ser Asn Ser Ile Gly Cys Arg Ile Thr Val Asn Gly Val Val
 115 120 125

aag gac gaa agg atc gtc aac gaa gtg cgc gcc tat acc ttc tgc ctc 432
 Lys Asp Glu Arg Ile Val Asn Glu Val Arg Ala Tyr Thr Phe Cys Leu
 130 135 140

gac aag tcc tca tga 447
 Asp Lys Ser Ser
 145

<210> 10
 <211> 148
 <212> PRT
 <213> Mycobacterium complex

<400> 10
 Val Gln Gly Ile Ser Val Thr Gly Leu Val Lys Arg Gly Trp Met Val
 1 5 10 15

Leu Val Ala Val Ala Val Val Ala Val Ala Gly Phe Ser Val Tyr Arg
 20 25 30

Leu His Gly Ile Phe Gly Ser His Asp Thr Thr Ser Thr Ala Gly Gly
 35 40 45

Val Ala Asn Asp Ile Lys Pro Phe Asn Pro Lys Gln Val Thr Leu Glu
 50 55 60

Val Phe Gly Ala Pro Gly Thr Val Ala Thr Ile Asn Tyr Leu Asp Val
 65 70 75 80

Asp Ala Thr Pro Arg Gln Val Leu Asp Thr Thr Leu Pro Trp Ser Tyr
 85 90 95

Thr Ile Thr Thr Thr Leu Pro Ala Val Phe Ala Asn Val Val Ala Gln
 100 105 110

Gly Asp Ser Asn Ser Ile Gly Cys Arg Ile Thr Val Asn Gly Val Val
 115 120 125

Lys Asp Glu Arg Ile Val Asn Glu Val Arg Ala Tyr Thr Phe Cys Leu
 130 135 140

Asp Lys Ser Ser
145

<210> 11
<211> 399
<212> DNA
<213> Mycobacterium complex

<220>
<221> CDS
<222> (1)..(399)

<400> 11
ctg gtt gcc gtg gcg gtg gtg gcg gtc gcg gga ttc agc gtc tat cgg 48
Leu Val Ala Val Ala Val Val Ala Val Ala Gly Phe Ser Val Tyr Arg
1 5 10 15
ttg cac ggc atc ttc ggc tcg cac gac acc acc tcg acc gcc ggt ggt 96
Leu His Gly Ile Phe Gly Ser His Asp Thr Thr Ser Thr Ala Gly Gly
20 25 30
gtc gcg aac gac atc aag ccg ttc aac ccc aaa cag gta acc ctc gag 144
Val Ala Asn Asp Ile Lys Pro Phe Asn Pro Lys Gln Val Thr Leu Glu
35 40 45
gtc ttt ggc gct ccc gga acc gtg gca acg atc aat tat ctg gac gtg 192
Val Phe Gly Ala Pro Gly Thr Val Ala Thr Ile Asn Tyr Leu Asp Val
50 55 60
gat gcc aca cct cgg caa gtc ctg gac acg acc ctg ccg tgg tca tac 240
Asp Ala Thr Pro Arg Gln Val Leu Asp Thr Thr Leu Pro Trp Ser Tyr
65 70 75 80
acg atc acg acg acc ctg ccc gcg gtc ttc gcc aat gtt gtc gcg caa 288
Thr Ile Thr Thr Thr Leu Pro Ala Val Phe Ala Asn Val Val Ala Gln
85 90 95
ggc gac agc aat tcc atc ggc tgc cgc atc acc gtc aac ggt gta gtc 336
Gly Asp Ser Asn Ser Ile Gly Cys Arg Ile Thr Val Asn Gly Val Val
100 105 110
aag gac gaa agg atc gtc aac gaa gtg cgc gcc tat acc ttc tgc ctc 384
Lys Asp Glu Arg Ile Val Asn Glu Val Arg Ala Tyr Thr Phe Cys Leu
115 120 125
gac aag tcc tca tga 399
Asp Lys Ser Ser
130

<210> 12
<211> 132
<212> PRT
<213> Mycobacterium complex

<400> 12

Leu Val Ala Val Ala Val Val Ala Val Ala Gly Phe Ser Val Tyr Arg
 1 5 10 15

Leu His Gly Ile Phe Gly Ser His Asp Thr Thr Ser Thr Ala Gly Gly
 20 25 30

Val Ala Asn Asp Ile Lys Pro Phe Asn Pro Lys Gln Val Thr Leu Glu
 35 40 45

Val Phe Gly Ala Pro Gly Thr Val Ala Thr Ile Asn Tyr Leu Asp Val
 50 55 60

Asp Ala Thr Pro Arg Gln Val Leu Asp Thr Thr Leu Pro Trp Ser Tyr
 65 70 75 80

Thr Ile Thr Thr Thr Leu Pro Ala Val Phe Ala Asn Val Val Ala Gln
 85 90 95

Gly Asp Ser Asn Ser Ile Gly Cys Arg Ile Thr Val Asn Gly Val Val
 100 105 110

Lys Asp Glu Arg Ile Val Asn Glu Val Arg Ala Tyr Thr Phe Cys Leu
 115 120 125

Asp Lys Ser Ser
 130

<210> 13

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 13

cggtcaaccc caaacaggta

20

<210> 14

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 14
 aatcgaactc gtggaacacc 20

<210> 15
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic primer

<400> 15
 attcagcgtc tatcggttgc 20

<210> 16
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic primer

<400> 16
 agcagctcgg gatatcgtag 20

<210> 17
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic primer

<400> 17
 ctacctcatc ttccggtcca 20

<210> 18
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic primer

<400> 18
 catagatccc ggacatggtg 20

```
<220>  
<221> CDS  
<222> (517)..(2307)
```

<400> 19																
gatcccgtcg		ccgcggcgct		ggagctggcc		gccggggccc		cagccgcccc		gcgcgaggtc						60
gtgctggcga		gcaaagccac		catgcgcgcc		acagccagcc		ccggatcgct		ggaccttgag						120
caacacgaac		tcgccaaacg		cttagaactt		gggcgcgagg		cgaaatcggt		ccagtcgccc						180
gagttcgccg		ctcgcttggc		tgccgctcaa		cacaggtagc		gcctaccagc		ctcgctggtt						240
tccatggcgt		gccccagtcc		gaagctgctg		ctgcttgact		ccgcgcgctg		ggcccgcgagc						300
cgcgctgttg		tacggcccaa		acggcgtgtc		ggtgtacagt		cgcgcgctcg		cggcttcagt						360
ccggcccccc		gactccggca		ggcccgcgag		cgcccagcgc		tagcccgaag		ttcccccttg						420
taggggcggg		ctgagtttcg		atctgtttcg		tgagcaggtg		tttctgtgtt		caacttcctt						480
caacatgtac		tcatgtatta		ttgagaatag		ctcggc		gtg	tca	tcc	tct	gat	gac			534
								Val	Ser	Ser	Ser	Asp	Asp			
								1					5			
gct att atc gcg ctg acc gcg tgt tat aaa gta atc atg tac att acc																582
Ala Ile Ile Ala Leu Thr Ala Cys Tyr Lys Val Ile Met Tyr Ile Thr																
		10				15				20						
cgg gta ccc aac cgg gga tcc ccg ccg gcg gtg ctg ttg cgg gaa agc																630
Arg Val Pro Asn Arg Gly Ser Pro Pro Ala Val Leu Arg Glu Ser																
		25				30				35						
ttc cgc gaa aac ggc aag gtc aag acg cgt acc ctg gcc aac ctc tca																678
Phe Arg Glu Asn Gly Lys Val Lys Thr Arg Thr Leu Ala Asn Leu Ser																
		40				45				50						
cgc tgg ccc gag cac aag ctg gac aga ctg gac cgg gcg ctt aag ggc																726
Arg Trp Pro Glu His Lys Leu Asp Arg Leu Asp Arg Ala Leu Lys Gly																
		55				60				65				70		
ttg ccg ccc gcg gac tgg gat cta gcc gag gcc ttc gat atc acc cgc																774
Leu Pro Pro Ala Asp Trp Asp Leu Ala Glu Ala Phe Asp Ile Thr Arg																
				75				80				85				
agc ctg ccg cac ggg cat gtg gcc gcg gtg gcc ggc acc gcc gag aag																822
Ser Leu Pro His Gly His Val Ala Ala Val Ala Gly Thr Ala Glu Lys																
				90				95				100				
ctg ggc ata ccc gag ctg atc gac ccc acc ccg tcg cgg cgg cgc aac																870
Leu Gly Ile Pro Glu Leu Ile Asp Pro Thr Pro Ser Arg Arg Arg Asn																
		105				110				115						

ctg gtg ctg gcc atg ctg atc ggg cag atc atc gag ccc gga tcg aaa	918
Leu Val Leu Ala Met Leu Ile Gly Gln Ile Ile Glu Pro Gly Ser Lys	
120 125 130	
ctg gcg atc gcg cgc ggg ctg cgc gcc cag acc gcc acc agc acg ctg	966
Leu Ala Ile Ala Arg Gly Leu Arg Ala Gln Thr Ala Thr Ser Thr Leu	
135 140 145 150	
ggc ggc gtg ctg ggt gtc tcg ggc gcc gat gag gac gac ctg tat gac	1014
Gly Ala Val Leu Gly Val Ser Gly Ala Asp Glu Asp Asp Leu Tyr Asp	
155 160 165	
gcg atg gac tgg gcg ctg gag cgc aaa gac ggc atc gaa aac gcc ttg	1062
Ala Met Asp Trp Ala Leu Glu Arg Lys Asp Gly Ile Glu Asn Ala Leu	
170 175 180	
gcc gca cgg cat ctg acc aac ggc acc ctg gtg ctc tat gac gta tcc	1110
Ala Ala Arg His Leu Thr Asn Gly Thr Leu Val Leu Tyr Asp Val Ser	
185 190 195	
tcg gcg gcg ttc gag ggc cac acc tgc ccg ctg gga gcg atc ggg cac	1158
Ser Ala Ala Phe Glu Gly His Thr Cys Pro Leu Gly Ala Ile Gly His	
200 205 210	
gcc cgc gac ggg gtc aaa ggc cgg ctg cag atc gtc tac ggg ctg ctg	1206
Ala Arg Asp Gly Val Lys Gly Arg Leu Gln Ile Val Tyr Gly Leu Leu	
215 220 225 230	
tgc tca ccc aag gga gcg ccg gtg gcc atc gag gtg ttc aag ggc aac	1254
Cys Ser Pro Lys Gly Ala Pro Val Ala Ile Glu Val Phe Lys Gly Asn	
235 240 245	
acc gcc gac ccg aaa act ctg aaa gct caa atc gac aag ctc aaa acc	1302
Thr Ala Asp Pro Lys Thr Leu Lys Ala Gln Ile Asp Lys Leu Lys Thr	
250 255 260	
cgg ttc ggg ttg acc cgc atc gcc ctg gtg ggc gat cgg ggc atg ctc	1350
Arg Phe Gly Leu Thr Arg Ile Ala Leu Val Gly Asp Arg Gly Met Leu	
265 270 275	
act tcc gcg cgc atc cgt gac gag ctg cgt ccg gcg cac ctg gat tgg	1398
Thr Ser Ala Arg Ile Arg Asp Glu Leu Arg Pro Ala His Leu Asp Trp	
280 285 290	
atc agc gcg ctg cgc gcc ccg cag atc aag atc ctg ctc gag gac ggg	1446
Ile Ser Ala Leu Arg Ala Pro Gln Ile Lys Ile Leu Leu Glu Asp Gly	
295 300 305 310	
gcg ctg cag ctg tcg ctg ttc gat gag cag aac ctg ttc gag atc act	1494
Ala Leu Gln Leu Ser Leu Phe Asp Glu Gln Asn Leu Phe Glu Ile Thr	
315 320 325	
cac ccc gac tat ccc ggt gag cgg ctg gtg tgc tgc cac aac ccc gcc	1542
His Pro Asp Tyr Pro Gly Glu Arg Leu Val Cys Cys His Asn Pro Ala	
330 335 340	

ctg gcc gac gag cgc gcc cgc aaa cgc gcc gag ctg ctg gcg gcc acc Leu Ala Asp Glu Arg Ala Arg Lys Arg Ala Glu Leu Leu Ala Ala Thr 345 350 355	1590
gaa aag gag ctg cag gcc atc gcc gaa gcc acc cgc cgc caa cgc cgg Glu Lys Glu Leu Gln Ala Ile Ala Glu Ala Thr Arg Arg Gln Arg Arg 360 365 370	1638
ccg tta cgc ggt aca gac aag atc ggc ctg cgg gtg ggc aag gtg cgc Pro Leu Arg Gly Thr Asp Lys Ile Gly Leu Arg Val Gly Lys Val Arg 375 380 385 390	1686
aac aag ttc aag atg gcc aag cac ttt gac ctg cac atc acc gat gag Asn Lys Phe Lys Met Ala Lys His Phe Asp Leu His Ile Thr Asp Glu 395 400 405	1734
gcc ttc agc ttc acc cgc aac cag aac agt atc gcc gcc gag gcc gcc Ala Phe Ser Phe Thr Arg Asn Gln Asn Ser Ile Ala Ala Glu Ala Ala 410 415 420	1782
ctc gac ggc atc tac gtg cta cgc acc agc ctg ccc gac aac gcc ctg Leu Asp Gly Ile Tyr Val Leu Arg Thr Ser Leu Pro Asp Asn Ala Leu 425 430 435	1830
ggc cgc gac gac gtg gtg ggc cgc tac aaa gac ctc gcc gac gtc gaa Gly Arg Asp Asp Val Val Gly Arg Tyr Lys Asp Leu Ala Asp Val Glu 440 445 450	1878
cgc ttc ttc cgc acc ctc aac agc gaa ctg gac gta cgc ccc atc cgg Arg Phe Phe Arg Thr Leu Asn Ser Glu Leu Asp Val Arg Pro Ile Arg 455 460 465 470	1926
cat cgg ctg gcc gac cgg gtc cgc gcc cac atg ttc ttg cac atg ctc His Arg Leu Ala Asp Arg Val Arg Ala His Met Phe Leu His Met Leu 475 480 485	1974
tcc tac tac atc agc tgg cac atg aaa caa gcc ctg gcc cca atc ctg Ser Tyr Tyr Ile Ser Trp His Met Lys Gln Ala Leu Ala Pro Ile Leu 490 495 500	2022
ttc acc gac aac gac aaa ccc gcc gcc gcc gcc aaa cgc gcc gac ccc Phe Thr Asp Asn Asp Lys Pro Ala Ala Ala Lys Arg Ala Asp Pro 505 510 515	2070
gtc gcg cca gcc caa cgc tcc gac gaa gcg ctg aac aag gca gca cgc Val Ala Pro Ala Gln Arg Ser Asp Glu Ala Leu Asn Lys Ala Ala Arg 520 525 530	2118
aaa cgc acc gaa gac aac caa ccg gtg cac agc ttc acc agc ctg ctc Lys Arg Thr Glu Asp Asn Gln Pro Val His Ser Phe Thr Ser Leu Leu 535 540 545 550	2166
acc gac ctg gcc acc atc tgc gcc aac tac atc caa ccc aca gac gac Thr Asp Leu Ala Thr Ile Cys Ala Asn Tyr Ile Gln Pro Thr Asp Asp 555 560 565	2214

ctg cca gca ttc acc aaa acc acc acc ccc acc ccc aca caa cgg cgc 2262
Leu Pro Ala Phe Thr Lys Thr Thr Thr Pro Thr Pro Thr Gln Arg Arg
570 575 580

gcc ttc gac cta ctg gcc gtt tcc cac cgc cac ggc ctg gcg tag 2307
Ala Phe Asp Leu Leu Ala Val Ser His Arg His Gly Leu Ala
585 590 595

tcagtaccga accacaaatg cccaggtcaa cgacacaaac cgcgccggat caggggggaac 2367

ttcgggctag ccgggcgcgc cgg 2390

<210> 20

<211> 596

<212> PRT

<213> Mycobacterium canettii

<400> 20

Val Ser Ser Ser Asp Asp Ala Ile Ile Ala Leu Thr Ala Cys Tyr Lys
1 5 10 15

Val Ile Met Tyr Ile Thr Arg Val Pro Asn Arg Gly Ser Pro Pro Ala
20 25 30

Val Leu Leu Arg Glu Ser Phe Arg Glu Asn Gly Lys Val Lys Thr Arg
35 40 45

Thr Leu Ala Asn Leu Ser Arg Trp Pro Glu His Lys Leu Asp Arg Leu
50 55 60

Asp Arg Ala Leu Lys Gly Leu Pro Pro Ala Asp Trp Asp Leu Ala Glu
65 70 75 80

Ala Phe Asp Ile Thr Arg Ser Leu Pro His Gly His Val Ala Ala Val
85 90 95

Ala Gly Thr Ala Glu Lys Leu Gly Ile Pro Glu Leu Ile Asp Pro Thr
100 105 110

Pro Ser Arg Arg Arg Asn Leu Val Leu Ala Met Leu Ile Gly Gln Ile
115 120 125

Ile Glu Pro Gly Ser Lys Leu Ala Ile Ala Arg Gly Leu Arg Ala Gln
130 135 140

Thr Ala Thr Ser Thr Leu Gly Ala Val Leu Gly Val Ser Gly Ala Asp
145 150 155 160

Glu Asp Asp Leu Tyr Asp Ala Met Asp Trp Ala Leu Glu Arg Lys Asp
 165 170 175

Gly Ile Glu Asn Ala Leu Ala Ala Arg His Leu Thr Asn Gly Thr Leu
 180 185 190

Val Leu Tyr Asp Val Ser Ser Ala Ala Phe Glu Gly His Thr Cys Pro
 195 200 205

Leu Gly Ala Ile Gly His Ala Arg Asp Gly Val Lys Gly Arg Leu Gln
 210 215 220

Ile Val Tyr Gly Leu Leu Cys Ser Pro Lys Gly Ala Pro Val Ala Ile
 225 230 235 240

Glu Val Phe Lys Gly Asn Thr Ala Asp Pro Lys Thr Leu Lys Ala Gln
 245 250 255

Ile Asp Lys Leu Lys Thr Arg Phe Gly Leu Thr Arg Ile Ala Leu Val
 260 265 270

Gly Asp Arg Gly Met Leu Thr Ser Ala Arg Ile Arg Asp Glu Leu Arg
 275 280 285

Pro Ala His Leu Asp Trp Ile Ser Ala Leu Arg Ala Pro Gln Ile Lys
 290 295 300

Ile Leu Leu Glu Asp Gly Ala Leu Gln Leu Ser Leu Phe Asp Glu Gln
 305 310 315 320

Asn Leu Phe Glu Ile Thr His Pro Asp Tyr Pro Gly Glu Arg Leu Val
 325 330 335

Cys Cys His Asn Pro Ala Leu Ala Asp Glu Arg Ala Arg Lys Arg Ala
 340 345 350

Glu Leu Leu Ala Ala Thr Glu Lys Glu Leu Gln Ala Ile Ala Glu Ala
 355 360 365

Thr Arg Arg Gln Arg Arg Pro Leu Arg Gly Thr Asp Lys Ile Gly Leu
 370 375 380

Arg Val Gly Lys Val Arg Asn Lys Phe Lys Met Ala Lys His Phe Asp
 385 390 395 400

Leu His Ile Thr Asp Glu Ala Phe Ser Phe Thr Arg Asn Gln Asn Ser
 405 410 415

Ile Ala Ala Glu Ala Ala Leu Asp Gly Ile Tyr Val Leu Arg Thr Ser
 420 425 430

Leu Pro Asp Asn Ala Leu Gly Arg Asp Asp Val Val Gly Arg Tyr Lys
 435 440 445

Asp Leu Ala Asp Val Glu Arg Phe Phe Arg Thr Leu Asn Ser Glu Leu
 450 455 460

Asp Val Arg Pro Ile Arg His Arg Leu Ala Asp Arg Val Arg Ala His
 465 470 475 480

Met Phe Leu His Met Leu Ser Tyr Tyr Ile Ser Trp His Met Lys Gln
 485 490 495

Ala Leu Ala Pro Ile Leu Phe Thr Asp Asn Asp Lys Pro Ala Ala Ala
 500 505 510

Ala Lys Arg Ala Asp Pro Val Ala Pro Ala Gln Arg Ser Asp Glu Ala
 515 520 525

Leu Asn Lys Ala Ala Arg Lys Arg Thr Glu Asp Asn Gln Pro Val His
 530 535 540

Ser Phe Thr Ser Leu Leu Thr Asp Leu Ala Thr Ile Cys Ala Asn Tyr
 545 550 555 560

Ile Gln Pro Thr Asp Asp Leu Pro Ala Phe Thr Lys Thr Thr Thr Pro
 565 570 575

Thr Pro Thr Gln Arg Arg Ala Phe Asp Leu Leu Ala Val Ser His Arg
 580 585 590

His Gly Leu Ala
 595

<210> 21
 <211> 1191
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <221> CDS
 <222> (1)..(1191)

<400> 21
 gtg cag ggg att tca gtg act ggc ctg gtc aaa cgc ggc tgg atg gtg 48
 Val Gln Gly Ile Ser Val Thr Gly Leu Val Lys Arg Gly Trp Met Val
 1 5 10 15

aga tcc gtc ttt gac acg atc gac ggt atc gac caa ctc ggc gag cag 96
 Arg Ser Val Phe Asp Thr Ile Asp Gly Ile Asp Gln Leu Gly Glu Gln
 20 25 30

ctg gcc agc gtg acc gta acc ttg gac aag ttg gct gcg atc cag cct 144
 Leu Ala Ser Val Thr Val Thr Leu Asp Lys Leu Ala Ala Ile Gln Pro
 35 40 45

caa ttg gtg gcg ctg cta cca gac gag atc gcc agc cag cag atc aat 192
 Gln Leu Val Ala Leu Leu Pro Asp Glu Ile Ala Ser Gln Gln Ile Asn
 50 55 60

cgg gaa ctg gcg ctg gct aac tac gcc acc atg tcc ggg atc tat gcc 240
 Arg Glu Leu Ala Leu Ala Asn Tyr Ala Thr Met Ser Gly Ile Tyr Ala
 65 70 75 80

cag acg gcg gcc ttg atc gaa aac gct gcc gcc atg gga caa gcc ttt 288
 Gln Thr Ala Ala Leu Ile Glu Asn Ala Ala Ala Met Gly Gln Ala Phe
 85 90 95

gac gcc gcc aag aac gac gac tcc ttc tat ctg ccg ccg gag gct ttt 336
 Asp Ala Ala Lys Asn Asp Asp Ser Phe Tyr Leu Pro Pro Glu Ala Phe
 100 105 110

gac aac cca gat ttc cag cgc ggc ctg aaa ttg ttc ctg tcg gca gac 384
 Asp Asn Pro Asp Phe Gln Arg Gly Leu Lys Leu Phe Leu Ser Ala Asp
 115 120 125

ggt aag gcg gct cgg atg atc atc tcc cat gaa ggc gat ccc gcc acc 432
 Gly Lys Ala Ala Arg Met Ile Ile Ser His Glu Gly Asp Pro Ala Thr
 130 135 140

ccc gaa ggc att tcg cat atc gac gcg atc aag cag gcg gcc cac gag 480
 Pro Glu Gly Ile Ser His Ile Asp Ala Ile Lys Gln Ala Ala His Glu
 145 150 155 160

gcc gtg aag ggc act ccc atg gcg ggt gct ggg atc tat ctg gcc ggc 528
 Ala Val Lys Gly Thr Pro Met Ala Gly Ala Gly Ile Tyr Leu Ala Gly
 165 170 175

acg gcc gcc acc ttc aag gac att caa gac ggc gcc acc tac gac ctc 576
 Thr Ala Ala Thr Phe Lys Asp Ile Gln Asp Gly Ala Thr Tyr Asp Leu
 180 185 190

ctg atc gcc gga ata gcc gcg ctg agc ttg att ttg ctc atc atg atg Leu Ile Ala Gly Ile Ala Ala Leu Ser Leu Ile Leu Leu Ile Met Met 195 200 205	624
atc att acc cga agc ctg gtt gcg gcg ctg gtg atc gtg ggc acg gtg Ile Ile Thr Arg Ser Leu Val Ala Ala Leu Val Ile Val Gly Thr Val 210 215 220	672
gcg ctg tcg ttg ggc gct tct ttt ggc ctg tcc gtg ctg gtg tgg cag Ala Leu Ser Leu Gly Ala Ser Phe Gly Leu Ser Val Leu Val Trp Gln 225 230 235 240	720
cat ctt ctc ggt atc cag ttg tac tgg atc gtg ctc gcg ctg gcc gtc His Leu Leu Gly Ile Gln Leu Tyr Trp Ile Val Leu Ala Leu Ala Val 245 250 255	768
atc ctg ctc ctg gcc gtg gga tcg gac tat aac ttg ctg ctg att tcc Ile Leu Leu Leu Ala Val Gly Ser Asp Tyr Asn Leu Leu Leu Ile Ser 260 265 270	816
cga ttc aag gag gag atc ggt gca ggt ttg aac acc ggc atc atc cgt Arg Phe Lys Glu Glu Ile Gly Ala Gly Leu Asn Thr Gly Ile Ile Arg 275 280 285	864
gcg atg gcc ggc acc ggc ggg gtg gtg acc gct gcc ggc ctg gtg ttc Ala Met Ala Gly Thr Gly Val Val Thr Ala Ala Gly Leu Val Phe 290 295 300	912
gcc gcc act atg tct tcg ttc gtg ttc agt gat ttg cgg gtc ctc ggt Ala Ala Thr Met Ser Ser Phe Val Phe Ser Asp Leu Arg Val Leu Gly 305 310 315 320	960
cag atc ggg acc acc att ggt ctt ggg ctg ctg ttc gac acg ctg gtg Gln Ile Gly Thr Thr Ile Gly Leu Gly Leu Leu Phe Asp Thr Leu Val 325 330 335	1008
gtg cgc gcg ttc atg acc ccg tcc atc gcg gtg ctg ctc ggg cgc tgg Val Arg Ala Phe Met Thr Pro Ser Ile Ala Val Leu Leu Gly Arg Trp 340 345 350	1056
ttc tgg tgg ccg caa cga gtg cgc ccg cgc cct gcc agc agg atg ctt Phe Trp Trp Pro Gln Arg Val Arg Pro Arg Pro Ala Ser Arg Met Leu 355 360 365	1104
cgg ccg tac ggc ccg cgg ccc gtg gtt cgt gaa ttg ctg ctg cgc gag Arg Pro Tyr Gly Pro Arg Pro Val Val Arg Glu Leu Leu Leu Arg Glu 370 375 380	1152
ggc aac gat gac ccg aga act cag gtg gct acc cac cgt Gly Asn Asp Asp Pro Arg Thr Gln Val Ala Thr His Arg 385 390 395	1191

<210> 22

<211> 397

<212> PRT

<213> Mycobacterium tuberculosis

<400> 22

Val Gln Gly Ile Ser Val Thr Gly Leu Val Lys Arg Gly Trp Met Val
 1 5 10 15

Arg Ser Val Phe Asp Thr Ile Asp Gly Ile Asp Gln Leu Gly Glu Gln
 20 25 30

Leu Ala Ser Val Thr Val Thr Leu Asp Lys Leu Ala Ala Ile Gln Pro
 35 40 45

Gln Leu Val Ala Leu Leu Pro Asp Glu Ile Ala Ser Gln Gln Ile Asn
 50 55 60

Arg Glu Leu Ala Leu Ala Asn Tyr Ala Thr Met Ser Gly Ile Tyr Ala
 65 70 75 80

Gln Thr Ala Ala Leu Ile Glu Asn Ala Ala Ala Met Gly Gln Ala Phe
 85 90 95

Asp Ala Ala Lys Asn Asp Asp Ser Phe Tyr Leu Pro Pro Glu Ala Phe
 100 105 110

Asp Asn Pro Asp Phe Gln Arg Gly Leu Lys Leu Phe Leu Ser Ala Asp
 115 120 125

Gly Lys Ala Ala Arg Met Ile Ile Ser His Glu Gly Asp Pro Ala Thr
 130 135 140

Pro Glu Gly Ile Ser His Ile Asp Ala Ile Lys Gln Ala Ala His Glu
 145 150 155 160

Ala Val Lys Gly Thr Pro Met Ala Gly Ala Gly Ile Tyr Leu Ala Gly
 165 170 175

Thr Ala Ala Thr Phe Lys Asp Ile Gln Asp Gly Ala Thr Tyr Asp Leu
 180 185 190

Leu Ile Ala Gly Ile Ala Ala Leu Ser Leu Ile Leu Leu Ile Met Met
 195 200 205

Ile Ile Thr Arg Ser Leu Val Ala Ala Leu Val Ile Val Gly Thr Val
 210 215 220

Ala Leu Ser Leu Gly Ala Ser Phe Gly Leu Ser Val Leu Val Trp Gln
 225 230 235 240

His Leu Leu Gly Ile Gln Leu Tyr Trp Ile Val Leu Ala Leu Ala Val
 245 250 255

Ile Leu Leu Leu Ala Val Gly Ser Asp Tyr Asn Leu Leu Leu Ile Ser
 260 265 270

Arg Phe Lys Glu Glu Ile Gly Ala Gly Leu Asn Thr Gly Ile Ile Arg
 275 280 285

Ala Met Ala Gly Thr Gly Gly Val Val Thr Ala Ala Gly Leu Val Phe
 290 295 300

Ala Ala Thr Met Ser Ser Phe Val Phe Ser Asp Leu Arg Val Leu Gly
 305 310 315 320

Gln Ile Gly Thr Thr Ile Gly Leu Gly Leu Leu Phe Asp Thr Leu Val
 325 330 335

Val Arg Ala Phe Met Thr Pro Ser Ile Ala Val Leu Leu Gly Arg Trp
 340 345 350

Phe Trp Trp Pro Gln Arg Val Arg Pro Arg Pro Ala Ser Arg Met Leu
 355 360 365

Arg Pro Tyr Gly Pro Arg Pro Val Val Arg Glu Leu Leu Leu Arg Glu
 370 375 380

Gly Asn Asp Asp Pro Arg Thr Gln Val Ala Thr His Arg
 385 390 395

<210> 23

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 primer

<400> 23

ggcctgggtca aacgcggctg gatgctg

<210> 24
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 24
 agatccgtct ttgacacgat cgacg 25

<210> 25
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 25
 gtcagccaag tcaggctacc 20

<210> 26
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 26
 gaaacagtcc ccagcaggt 19

<210> 27
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 27
 caacgttggtg gttggtgagg 20

<210> 28
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic primer

 <400> 28
 ttcaacgggt tactgcgaat 20

 <210> 29
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic primer

 <400> 29
 tatagctctc ggcaggttcc 20

 <210> 30
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic primer

 <400> 30
 ctcgaccgcg acgatgtgc 19

 <210> 31
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic primer

 <400> 31
 atcggcatct atgtcggtgt 20

 <210> 32
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic primer

 <400> 32
 cctcgttgtc accgcgtatg 20

<210> 33
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 33
 ttatcttggc gttgacgatg

20

<210> 34
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 34
 ctgacgtcgt tgtcgaggta

20

<210> 35
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 35
 catataaggg tgcccgtac

20

<210> 36
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 36
 gtacccccag gcgatctt

18

<210> 37
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

 <400> 37
 caaggggtat gaggttcacg 20

 <210> 38
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 primer

 <400> 38
 ctcgtcgaag gccactaaag 20

 <210> 39
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 primer

 <400> 39
 cggtgattcg tgattgaaca 20

 <210> 40
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 primer

 <400> 40
 aaggcgaaca gattcagcat 20

 <210> 41
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 41
 aatcacgctg ctgctactcc 20

<210> 42
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic primer

<400> 42
 caagttgggt ctggtcgaat 20

<210> 43
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic primer

<400> 43
 gtgcttttgc ctcttggtc 19

<210> 44
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic primer

<400> 44
 gctaccaag gtctcctggt 20

<210> 45
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic primer

<400> 45
 cagctggtga gttcaaagtc 20

<210> 46
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 46
 ctcccgacac ctgttcgt 18

<210> 47
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 47
 tggattgtcg acggtatgaa 20

<210> 48
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 48
 ggtaatcgtg gccgacaag 19

<210> 49
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 49
 ggtcgataag gtcacggaac 20

<210> 50
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic primer

 <400> 50
 cagctcttcc cctctcgac 19

 <210> 51
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic primer

 <400> 51
 ggtgtgattt ggtgagacga tg 22

 <210> 52
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic primer

 <400> 52
 caatcagggc tgtgctaacc 20

 <210> 53
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic primer

 <400> 53
 agttcctcct gactaatcca ggc 23

 <210> 54
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic primer

 <400> 54
 cgacagttgt gcgtactggt 20

<210> 55
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 55
 cgatgggtcaa caccactacg

20

<210> 56
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 56
 gtgtaggtca gccccatcc

19

<210> 57
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 57
 ctggacctcg atgaccactc

20

<210> 58
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 58
 gcccaacagc tcgacatc

18

<210> 59
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 59
gtaaccgctt caccggaat 19

<210> 60
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 60
ctgcaaccat ccggtacac 19

<210> 61
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 61
gtcaactcca cggaaagacc 20

<210> 62
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 62
gtcatgaacg ccggacag 18

<210> 63
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 63 cggcagctag acgacctc	18
<210> 64 <211> 20 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic primer	
<400> 64 tcacataggg gctgcgatag	20
<210> 65 <211> 20 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic primer	
<400> 65 aacgtgctgc gataggtttt	20
<210> 66 <211> 20 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic primer	
<400> 66 agaggaacct ttcggtggtt	20
<210> 67 <211> 20 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic primer	
<400> 67 gaaatacgag tgcgctgacc	20

<210> 68
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 68
 gccatcaacg tcaagaacct 20

<210> 69
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 69
 ctctgaacca tcggtgtcg 19

<210> 70
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 70
 cggccaggta acaaggagt 19

<210> 71
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 71
 ggatgtcact cggaacggca 20

<210> 72
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 72
 cgatggtggt tcttggtgag 20

<210> 73
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 73
 caccgggctg atcgagcga 19

<210> 74
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 74
 ggatcggctc agtgaatacc 20

<210> 75
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 75
 gtggagcacc ttgacctgat 20

<210> 76
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 76
 ttgattcgcc aacaactgaa 20

<210> 77
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 primer

<400> 77
 cgtcgaatac gagtcgaaca

20

<210> 78
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 primer

<400> 78
 gggctgggta gtgtcgattc

20

<210> 79
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 primer

<400> 79
 agcgcgtcga acaccggc

18

<210> 80
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 primer

<400> 80
 gagccactcc gatgttgact

20

<210> 81
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic primer

 <400> 81
 cctgaatccg cgcaattcca t 21

 <210> 82
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic primer

 <400> 82
 cacggaacc ctacctacat 20

 <210> 83
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic primer

 <400> 83
 gttctcctgt cgaacctcca 20

 <210> 84
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic primer

 <400> 84
 ggacggtgac ggtatttgtc 20

 <210> 85
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic primer

<400> 85
 acttcaccgg tttcatctcg 20

<210> 86
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 86
 tcgccaactt ctatggacct 20

<210> 87
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 87
 atcgatcagg tcgtcaatgc 20

<210> 88
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 88
 aaaccatgca gcgtctgcca 20

<210> 89
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 89
 acgccaccat caagatcc 18

<210> 90
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 90
 gcgtttctgc gtctggttga

20

<210> 91
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 91
 gggtgccaac gttaccgatg c

21

<210> 92
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 92
 ccggtggtgg tggcggct

18

<210> 93
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 93
 gggttcacgt tcattactgt tc

22

<210> 94
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

 <400> 94
 cccatcgtgg tcgttcacc 19

<210> 95
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

 <400> 95
 cctgcgctta tctctagcgg 20

<210> 96
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

 <400> 96
 gtaccgcgac cacctgctg 19

<210> 97
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

 <400> 97
 cgttcaaccc caaacaggta 20

<210> 98
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

 <400> 98
 ctacctcatc ttccggtcca 20

<210> 99
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 primer

 <400> 99
 aatcgaactc gtggaacacc 20

 <210> 100
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 primer

 <400> 100
 catagatccc ggacatggtg 20

 <210> 101
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 primer

 <400> 101
 ctaccagcac cgtcattctca 20

 <210> 102
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 primer

 <400> 102
 acaagctgat ccaccgagac 20

 <210> 103
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 103
aggtcgtatg gacgaacacc 20

<210> 104
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 104
gttcgtgtgt tgcgtcaagt 20

<210> 105
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 105
cgggtgctct atgcaatggt 20

<210> 106
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 106
cagctgggtg tgcttgtaaa 20

<210> 107
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 107
 tatgcatca ggcgtacttg 20

<210> 108
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic primer

<400> 108
 caaagcagtg gttcagcagt 20

<210> 109
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic primer

<400> 109
 caaagcagtg gttcagcagt 20

<210> 110
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic primer

<400> 110
 atcaggagct gcaaaccaac 20

<210> 111
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic primer

<400> 111
 ggcgtcatgg accctatc 20

<210> 112
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 112
 ggcgtcatgg accctatatc 20

<210> 113
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 113
 gtatcagagg gaccgagcag 20

<210> 114
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 114
 gtatcagagg gaccgagcag 20

<210> 115
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 115
 catagatccc ggacatggtg 20

<210> 116
 <211> 48
 <212> DNA
 <213> Mycobacterium bovis

<400> 116
ggcctgggcc gcggctggtg gtgctggttg ccgtggcggt ggtggcgg 48

<210> 117
<211> 42
<212> DNA
<213> Mycobacterium tuberculosis

<400> 117
ggcctgggcc gcggctggtg gtggccgctc ttgcccgtcg cg 42